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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 03:27:51 ; Search time 349 Seconds
(without alignments)
12708.216 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccccattggggc.....ctctdgcagatcaagtact 7992

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A_COMB.seq*
- 2: /cgn2_6/prodata/2/ina/5B_COMB.seq*
- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq*
- 5: /cgn2_6/prodata/2/ina/6C_COMB.seq*
- 6: /cgn2_6/prodata/2/ina/6D_COMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	7982.6	99.9	7989	4	US-09-539-601-10	Sequence 10, Appl
2	7960.6	99.6	8001	4	US-09-539-601-7	Sequence 7, Appl
3	7943	99.4	8001	4	US-09-539-601-22	Sequence 22, Appl
4	7941.4	99.4	8001	4	US-09-539-601-16	Sequence 16, Appl
5	7935	99.3	8001	4	US-09-539-601-28	Sequence 28, Appl
6	7324.6	91.6	8637	4	US-09-539-601-4	Sequence 4, Appl
7	7302.6	91.4	8649	4	US-09-539-601-13	Sequence 13, Appl
8	6180.4	77.3	11076	4	US-09-539-601-1	Sequence 1, Appl
9	6162.8	77.1	11076	4	US-09-539-601-25	Sequence 25, Appl
10	6161.2	77.1	11076	4	US-09-539-601-19	Sequence 19, Appl
11	6154.8	77.0	11076	4	US-09-539-601-31	Sequence 31, Appl
12	5312	66.5	9595	3	US-09-014-416-4	Sequence 4, Appl
13	5218	65.3	7917	3	US-08-324-977-31	Sequence 31, Appl
14	5218	65.3	7917	2	US-08-384-616-31	Sequence 31, Appl
15	5218	65.3	7917	2	US-08-304-686A-31	Sequence 31, Appl
16	5218	65.3	7917	3	US-09-315-850-31	Sequence 31, Appl
17	5218	65.3	9416	1	US-08-324-977-1	Sequence 1, Appl
18	5218	65.3	9416	2	US-08-384-616-1	Sequence 1, Appl
19	5218	65.3	9416	3	US-08-904-686A-1	Sequence 1, Appl
20	5218	65.3	9416	3	US-09-315-850-1	Sequence 1, Appl
21	5218	65.3	9416	4	US-08-823-895A-27	Sequence 27, Appl
22	5205.4	65.1	9472	4	US-08-150-204E-96	Sequence 96, Appl
23	5175.2	64.8	7863	1	US-08-324-977-35	Sequence 35, Appl
24	5175.2	64.8	7863	2	US-08-384-616-35	Sequence 35, Appl
25	5175.2	64.8	7863	2	US-08-904-686A-35	Sequence 35, Appl
26	5175.2	64.8	7863	3	US-09-315-850-35	Sequence 35, Appl
27	5175.2	64.8	9030	1	US-08-324-977-13	Sequence 13, Appl

28 5175.2 64.8 9030 2 US-08-384-616-13 Sequence 13, Appl
29 5175.2 64.8 9030 2 US-08-904-686A-13 Sequence 13, Appl
30 5175.2 64.8 9030 3 US-09-315-850-13 Sequence 13, Appl
31 4100.6 51.3 9599 3 US-09-014-416-2 Sequence 2, Appl
32 4099 51.3 9599 3 US-09-014-416-6 Sequence 6, Appl
33 4094.6 51.2 9646 3 US-08-811-566-1 Sequence 1, Appl
34 4094.6 51.2 9646 4 US-09-034-756-1 Sequence 1, Appl
35 4091 51.2 12980 3 US-08-811-566-5 Sequence 5, Appl
36 4091 51.2 12980 4 US-09-034-756-5 Sequence 5, Appl
37 4018.2 50.3 9379 3 US-08-388-874-1 Sequence 1, Appl
38 4018.2 50.3 9379 4 US-09-916-359-1 Sequence 1, Appl
39 4018.2 50.3 9401 1 US-07-910-760-9 Sequence 9, Appl
40 4018.2 50.3 9401 1 US-08-440-519-9 Sequence 9, Appl
41 4018.2 50.3 9401 4 US-08-440-549-9 Sequence 9, Appl
42 4018.2 50.3 9401 4 US-08-823-895A-25 Sequence 25, Appl
43 4017.4 50.3 9401 5 PCT-US91-02225-9 Sequence 9, Appl
44 4016.2 50.3 9379 3 US-08-444-818-176 Sequence 176, Appl
45 3967.2 49.6 9416 3 US-08-811-566-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-539-601-10

; Sequence 10, Application US/09539601C

; Patent No. 6630343

; GENERAL INFORMATION:

; APPLICANT: Bartschlagler, Ralf FW

; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System

; FILE REFERENCE: all sequences

; CURRENT APPLICATION NUMBER: US/09/539,601C

; CURRENT FILING DATE: 2001-08-30

; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY

; EARLIER FILING DATE: 1999-04-03

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 10

; LENGTH: 7989

; TYPE: DNA

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: (1)..(341)

; OTHER INFORMATION: construct I377/NS3-3'/wt

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (342)..(1181)

; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase

; OTHER INFORMATION: fusion protein

; FEATURE:

; NAME/KEY: RBS

; LOCATION: (1190)..(1800)

; OTHER INFORMATION: internal ribosome entry site from

; OTHER INFORMATION: encephalomyocarditis virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1801)..(7758)

; OTHER INFORMATION: hepatitis C virus NS3 - 5B

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: (7759)..(7989)

; PUBLICATION INFORMATION:

; AUTHORS: Lohmann, Volker

; AUTHORS: Krner, Frank

; AUTHORS: Koch, Jan-Oliver

; AUTHORS: Herian, Ulrike

; AUTHORS: Theilmann, Lorenz

; AUTHORS: Bartschlagler, Ralf

; TITLE: Replication of subgenomic hepatitis c virus RNAs in a

; JOURNAL: Science

; VOLUME: 285

;
i;
US-09-539-601-10

PAGES: 110-113

DATE: 1999-07-02

Matches 7985; Conservative

Query Match 99.9%; Score 7982.6; DB 4; Length 7989;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 181 GACGACGGGTCTCTTCTTGATCAACCGCTCAATGCTCGAGATTTGGGGTGGCCCC 240
Db 181 GACGACGGGTCTCTTCTTGATCAACCGCTCAATGCTCGAGATTTGGGGTGGCCCC 240
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Qy 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGCTCTGTAGCGACCTTTGAGGCGAGCGG 1500
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Db 1621 TGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGAGTGCAGAGGCTACCCATTGT 1680
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Qy 1741 AACGCTTAGGCGCCCGGAAACACCGGGAGCTGTTTCTTTGAAAAACAGATATACC 1800
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Qy 1801 ATGGCGCTATTAGCGCTTCTCCCAACAGACGCGAGGCTACTTGGCTGATCATCACT 1860
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Qy 1861 AGCTTCAAGGCGGGAACAGGAAACAGGTGAGGGGAGGTCGAGGCTCTCCACCGCA 1920
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Qy 1921 ACACAACTTTCTGCGGCTCAATGCGTGTCTTGAGTGTCTATCATGCTGCC 1980
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Db 1981 GGCTCAAAAGACCTTTGCGGCGCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
Qy 2041 CAGGACCTCTGCTGGTGGCAAGCGCCCGGGGGCGCTTCTTGACACCATGCACTGCG 2100

2041	Db	CAGGACCTCTGTCGGCTGGCAAGAGCGCCCCCGGGGCGGTTCCTTTGACCACTGACACTGC	2101
2101	Qy	GGCAGCTCGGACCTTTACTTGGTCA CGAGGCATGCCGATGTCACTTCGGGTGCGCGCGG	2160
	Db	GGCAGCTCGGACCTTTACTTGGTCA CGAGGCATGCCGATGTCACTTCGGGTGCGCGCGG	2160
	Qy	GGCAGCAGCAGGGGAGGCTACTCTCCCCAGGCGCGTCTCTACTTTGAAGGGCTCTTCG	2220
2161	Db	GGCAGACAGCAGGGGAGGCTACTCTCCCCAGGCGCGTCTCTACTTTGAAGGGCTCTTCG	2220
2221	Qy	GGGGTCCACTGCTCTGCCCTCGGGGCA CGCTGTGGGCATCTTTGGGCTCGGTGTGC	2280
	Db	GGGGTCCACTGCTCTGCCCTCGGGGCA CGCTGTGGGCATCTTTGGGCTCGGTGTGC	2280
	Qy	ACCGAGGGGTGCGAAGGGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
2281	Db	ACCGAGGGGTGCGAAGGGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
2341	Qy	CGGTCCCGGTCTTCA CGGCAAACTCTGCCCTCGGGCGGTACCGCAGACATTCAGGTG	2400
	Db	CGGTCCCGGTCTTCA CGGCAAACTCTGCCCTCGGGCGGTACCGCAGACATTCAGGTG	2400
	Qy	GCCCATCTACAGCCCTACTCTGTAGCGGCAAGGACATAAGGTGCGGCTCGGTATGCA	2460
2401	Db	GCCCATCTACAGCCCTACTCTGTAGCGGCAAGGACATAAGGTGCGGCTCGGTATGCA	2460
2461	Qy	GCCCAAGGGTATAAGGTGCTGTCTGAAACCGCTCGTCGCCGCGCACCTTAGTTCGGG	2520
	Db	GCCCAAGGGTATAAGGTGCTGTCTGAAACCGCTCGTCGCCGCGCACCTTAGTTCGGG	2520
	Qy	GGGTATATGTCTAAGGCACATGTGTACGCCCTAAACATCAGAACCGGGTAAAGCAATC	2580
2521	Db	GGGTATATGTCTAAGGCACATGTGTACGCCCTAAACATCAGAACCGGGTAAAGCAATC	2580
2581	Qy	ACCAGGGTGGCCCCATCAGCTACTCCACTATGGCAAGTTTCTGCCGAGCGGTGTTGC	2640
	Db	ACCAGGGTGGCCCCATCAGCTACTCCACTATGGCAAGTTTCTGCCGAGCGGTGTTGC	2640
	Qy	CTCTGGGGCGCCTATGACATCAATAATGTGATGAGTGCCACTCAACTGACTCGACCACT	2700
2641	Db	CTCTGGGGCGCCTATGACATCAATAATGTGATGAGTGCCACTCAACTGACTCGACCACT	2700
2701	Qy	ATCCTGGGCATCGGCA CAGTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTG	2760
	Db	ATCCTGGGCATCGGCA CAGTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTG	2760
	Qy	CTGCCACCGCTAGCCTCGCGATCGGTACCGTGCACATCCAAACATCGAGGAGGTG	2820
2761	Db	CTGCCACCGCTAGCCTCGCGATCGGTACCGTGCACATCCAAACATCGAGGAGGTG	2820
2821	Qy	GCTCTGTCCAGCACTGGAGAAATCCCCCTTTATGGCAAGCCATCCCCATCGAGACCACT	2880
	Db	GCTCTGTCCAGCACTGGAGAAATCCCCCTTTATGGCAAGCCATCCCCATCGAGACCACT	2880
	Qy	AAGGGGGAGGCA CTTCTATTCTGCGATTCCAAAGAGAAATGTGATGAGTTCGCGCG	2940
2881	Db	AAGGGGGAGGCA CTTCTATTCTGCGATTCCAAAGAGAAATGTGATGAGTTCGCGCG	2940
2941	Qy	AGCTCTCGGGCTCGGACTCAATGTGTAGCATATATACGGGGCCCTGATGTATCCGTG	3000
	Db	AGCTCTCGGGCTCGGACTCAATGTGTAGCATATATACGGGGCCCTGATGTATCCGTG	3000
	Qy	ATACCAACTAGCGGAGAGCTATTGTCTGTAGCAACGACGCTCTAATGACGGGCTTTACC	3060
3001	Db	ATACCAACTAGCGGAGAGCTATTGTCTGTAGCAACGACGCTCTAATGACGGGCTTTACC	3060
3061	Qy	GGCGATTTGCACTCAGTGTATCGACTCGAATACATGTGTACCCAGACAGTTCGACTTCAG	3120
	Db	GGCGATTTGCACTCAGTGTATCGACTCGAATACATGTGTACCCAGACAGTTCGACTTCAG	3120
	Qy	CTGGA CCGGACCTTCA CCAATTTGAGACGACGACCGTGCACAGACCGGGTGTCAOCTCG	3180
3121	Db	CTGGA CCGGACCTTCA CCAATTTGAGACGACGACCGTGCACAGACCGGGTGTCAOCTCG	3180

Qy	3181	CAGCGGAGGACAGGATGTGTAGGGGAGAGATGGGCATTTACAGGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGGAGGACAGGATGTGTAGGGGAGAGATGGGCATTTACAGGTTTGTGACTCCAGGA	3240
Qy	3241	GAA CGGCGCTCGGCATGTTGCAATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGGCTGT	3300
Db	3241	GAA CGGCGCTCGGCATGTTGCAATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGGCTGT	3300
Qy	3301	GCTTGGTATCAGAGCTACGCCCGCGGAGACCTCAGTTAGGTTGGGGGCTTACCTTAAACACA	3360
Db	3301	GCTTGGTATCAGAGCTACGCCCGCGGAGACCTCAGTTAGGTTGGGGGCTTACCTTAAACACA	3360
Qy	3361	CCAGGTTGCCCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGGCTCTTTTACAGGCTTC	3420
Db	3361	CCAGGTTGCCCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGGCTCTTTTACAGGCTTC	3420
Qy	3421	ACCCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGCAGGAGACAATTTCCCTCTAC	3480
Db	3421	ACCCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGCAGGAGACAATTTCCCTCTAC	3480
Qy	3481	CTGTTAGCATACAGGCTACGGTGTGCGCGCAGGCTCAGGCTCCACCTCCATCGTGGGAC	3540
Db	3481	CTGTTAGCATACAGGCTACGGTGTGCGCGCAGGCTCAGGCTCCACCTCCATCGTGGGAC	3540
Qy	3541	CAAAATGGGAAGTGTCTCATACGCTAAAGCCTACGCTGCACGGGCGCAACGCCCTCTGCTG	3600
Db	3541	CAAAATGGGAAGTGTCTCATACGCTAAAGCCTACGCTGCACGGGCGCAACGCCCTCTGCTG	3600
Qy	3601	TATAGGCTGGGAGCGGTTCAAACGAGGTTACTACACACACACCCCATTAACCAATACATC	3660
Db	3601	TATAGGCTGGGAGCGGTTCAAACGAGGTTACTACACACACACCCCATTAACCAATACATC	3660
Qy	3661	ATGCGATGATGTGCGCTGACCTGGAGTTCGTACAGAGCACTCGGTGCTGTAGGCGGA	3720
Db	3661	ATGCGATGATGTGCGCTGACCTGGAGTTCGTACAGAGCACTCGGTGCTGTAGGCGGA	3720
Qy	3721	GTCTAGCAGCTCTGGCGCGGTATTGCTGTGAACAAGGCAGCGTGTGTCATTGTGGGCGAGG	3780
Db	3721	GTCTAGCAGCTCTGGCGCGGTATTGCTGTGAACAAGGCAGCGTGTGTCATTGTGGGCGAGG	3780
Qy	3781	ATCATCTTGTCCGGAATGCGCGGCATCATTCCTCGGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Db	3781	ATCATCTTGTCCGGAATGCGCGGCATCATTCCTCGGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Qy	3841	GATGAGATGAAGAGTGCCTCACAACCTCCCTTACATCGAACAGGGAATGCAAGCTCGCC	3900
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Qy	3901	GAA CAATTCAAACAGAGGCAATCGGGTGTGTCGCAACAGCCACCAAGCAAGCGGAGGCT	3960
Db	3901	GAA CAATTCAAACAGAGGCAATCGGGTGTGTCGCAACAGCCACCAAGCAAGCGGAGGCT	3960
Qy	3961	GCTGTCTCCGTGTGGAATCCAAAGTGGCGGACCCCTCGAAGCCTTCTGGGCGAAGCATATG	4020
Db	3961	GCTGTCTCCGTGTGGAATCCAAAGTGGCGGACCCCTCGAAGCCTTCTGGGCGAAGCATATG	4020
Qy	4021	TGGAATTTTCAACAGCGGATACAAATTTTAGCAGGCTGTGTCACCTGCTGCTGCAACCCC	4080
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Qy	4081	GCATAGCATCATGATGGCATTCACAGCCTCTATCACACAGCCCGCTCACCAACCCAAACAT	4140
Db	4081	GCATAGCATCATGATGGCATTCACAGCCTCTATCACACAGCCCGCTCACCAACCCAAACAT	4140
Qy	4141	ACCCTCCTGTTTAAACATCTGGGGGGATGGGTGGCGGCCCAACTTGTCTCTCTCCACGCGCT	4200
Db	4141	ACCCTCCTGTTTAAACATCTGGGGGGATGGGTGGCGGCCCAACTTGTCTCTCTCCACGCGCT	4200
Qy	4201	GCTTCTGCTTTCTGTAGCGCGCGGCATCGCTGAGCGGCTGTGTGGCGAATAGCGCTTGGG	4260
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DB 4921 ACCAGGGCCCTGACGCCCTCCCGGCGCCAAATTTATCTAGGGCGCTGTGGGGGTG 4980
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DB 5101 GATGGGTGCGGTTCACAGGTACGCTCCAGCGTGCBAACCCCTCTCTACGGGAGGAGTTC 5160
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DB 5221 CCGGAGTACAGTGTCTACTTCCATGTACCGACCCCTTCCACATTAACGGCGGAGAGG 5280
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DB 5281 GCTTAAGCTGAGTGTGAGGAGGATCTCCCGCTCTGTGGCGAGCTCATCAGTACCCAG 5340
QY 5341 CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCCGTCTATGCTCTCCCGGACGCTGAC 5400

DB 5341 CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCCGTCTATGCTCTCCCGGACGCTGAC 5400
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6541	Db	ATGGGCTCTTCATACGGATTCCAAATCTCTCTCGACAGCGGTCGAGTTCCTGGTGAAT	6600
6601	Qy	GCTTGGAAAGCGAAATGCCCTTATGGGCTTCGCAATATGACACCCGCTGTTTGGACTCA	6660
6601	Db	GCTTGGAAAGCGAAATGCCCTTATGGGCTTCGCAATATGACACCCGCTGTTTGGACTCA	6660
6661	Qy	ACGGTCACTGAGAAATGACATCCGTTTGGAGAGTCAATCTACCAATGTTGTGACTTGGCC	6720
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6721	Db	CCCGAAGCCGACAGGCCATAAGTGCCTCACAGAGCGGCTTTATACGCGGGGCCCCCTG	6780
6781	Qy	ACTAATTTCTAAAGGCGAAACTCGCGCTATCGCCGGTCCGCGGAGCGGCTACTGACG	6840
6781	Db	ACTAATTTCTAAAGGCGAAACTCGCGCTATCGCCGGTCCGCGGAGCGGCTACTGACG	6840
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6841	Db	ACCACTGCGGTAAATACCCCTCACATGTTACTTGAAGGCCGCTCGCGGCTCTCGAGCTGCG	6900
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6901	Db	AACTCCAGGACTGCAGATGCTCGTATGGGAGACGACCTTGTGCTTATCTGTGAAAGC	6960
6961	Qy	CGCGGGACCCAGAGGACGAGCGCTACGGGCTTACGGAGGCTATGACTAGATAC	7020
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7081	Db	TCTTCCAAATGTCTAGTCGGGACGATGCAATCTGGCAAAAGGCTGACTATCTCACCCGT	7140
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7201	Qy	TCTTGCTAGGCAACATCATATGATGCGCCACACCTTGTGGCAAGGATGATCTGATG	7260
7201	Db	TCTTGCTAGGCAACATCATATGATGCGCCACACCTTGTGGCAAGGATGATCTGATG	7260
7261	Qy	ACTCATTTCTTCCATCCTTCTAGCTCAGGAAACAATTTGAAAAGCCCTAGATTGTACG	7320
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7321	Qy	ATCTACGGGCTGTTTACTTCCATTGAGCACTTGACCTACCTCAGATCAATTCAAAGCTC	7380
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7381	Qy	CATGGCCTTAGCGCATTTTCACTCCA TAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
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7501	Qy	GTCGCGCTTAGGCTACTGTCCCAAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
7501	Db	GTCGCGCTTAGGCTACTGTCCCAAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560

RESULT 2

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; Sequence 7, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3-5B
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)

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Query Match 99.6%; Score 7960.6; DB 4; Length 8001;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 12; Gaps 1;
QY 1 GCCAGCCCCCATTTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTCTG 60
DB 1 GCCAGCCCCCATTTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTCTG 60
QY 61 TCTTCACGACGAAAGCGCTAGCCATGCGTTAGTATGAGTGTCTGTCAGAGCTCCAGGAC 120
DB 61 TCTTCACGACGAAAGCGCTAGCCATGCGTTAGTATGAGTGTCTGTCAGAGCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAAATGGCCAG 180
DB 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAAATGGCCAG 180
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QY 241 GCGAGCTGTAGCGAGTGTGGTGGCGGAAAGGCTTGTGGTACTGCTGATAGG 300
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DB 301 GTGCTTGGAGTGCCTCGGAGGCTCTGTAGACCGGTGCAACATGAGCAGCAATCTTAAC 360
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DB 361 CTCGAAGAAACCAAA-----GGGGCGCCATGATGAACAGATGATTCG 420
QY 409 ACGGAGTCTCCGGCGCTTGGGTGGAGGCTATTGGCTATGACTGGGCACACAGA 468
DB 421 ACGGAGTCTCCGGCGCTTGGGTGGAGGCTATTGGCTATGACTGGGCACACAGA 480
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DB 841 TGGAGCCGGTCTTGTGATCAGCATGATCTGGACGAGAGCATCAGGGGCTCGCGCCAG 900
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DB 901 CCGAACCTGTTGCGCAGGCTCAAGGCGCGCATGCGCGAGGAGATCTCTGCTGACCC 960
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DB 1501 TCGAGCGAGCGAAACCCCGCTCTGCGACAGTCTCTGCGCGCAAAAGCACGCTGTA 1560
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DB 1561 TAAGATACACCTGCAAGGCGGCAACCCCGCTCTGAGTGGATAGTGTG 1620
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QY 1849 TGCATCATCACTAGCTCTCAGGCGCGGACAGGAAACAGGTTCGAGGGGAGGTTCAGGTG 1908
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Db	1921	GTCTCCACGCAACACAATCTTTCTCTGCGACCTCGCTCAATGCGGTGTGTGACGTGC	1980
Qy	1969	TATCATGTGTCGGGTCTAAAGACCCCTTCCGCGCCCAAGGGCCCAATCACCCTCAATGTAC	2028
Db	1981	TATCATGTGTGTCGGGTCTAAAGACCCCTTCCGCGCCCAAGGGCCCAATCACCCTCAATGTAC	2040
Qy	2029	ACCAATGTGACCAAGGAACTCGTGTGGCTGCGAAGCGGCCCGCGGGCGCGTTCTTGACA	2088
Db	2041	ACCAATGTGACCAAGGAACTCGTGTGGCTGCGAAGCGGCCCGCGGGCGCGTTCTTGACA	2100
Qy	2089	CCATGCACTCTGCGGCGAGCTCGGACCTTTACTTTGGTTCAGAGGCATGCCGATGCAATTCG	2148
Db	2101	CCATGCACTCTGCGGCGAGCTCGGACCTTTACTTTGGTTCAGAGGCATGCCGATGCAATTCG	2160
Qy	2149	GTGCGCGGCGGGGCGACAGCAGGGGGAGCCCTACTCTCCCCCAGGCGCGTCTCTACTTTG	2208
Db	2161	GTGCGCGGCGGGGCGACAGCAGGGGGAGCCCTACTCTCCCCCAGGCGCGTCTCTACTTTG	2220
Qy	2209	AAGGCTCTTCTGGGCGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTCTTCGG	2268
Db	2221	AAGGCTCTTCTGGGCGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTCTTCGG	2280
Qy	2269	GCTGCCGTGTGACCCGAGGGGTTCGAAAGGCGGTGGACTTTGTACCGCTCGAGTCTATG	2328
Db	2281	GCTGCCGTGTGACCCGAGGGGTTCGAAAGGCGGTGGACTTTGTACCGCTCGAGTCTATG	2340
Qy	2329	GAAGCACTATGCGGTCTCCCGTCTTCAOGGACAACTCGTCCCTCCGGCGGTACCGCAG	2388
Db	2341	GAAGCACTATGCGGTCTCCCGTCTTCAOGGACAACTCGTCCCTCCGGCGGTACCGCAG	2400
Qy	2389	ACATTCAGGTGGCCCATCTACAGCCCTTACTGTGTAGCGGCAAGACACTAAGGTGCGG	2448
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Qy	2449	GCTCGTATGCAAGCCCAAGGATTAAGGTGCTGTCTGTAACCCCTCGTCCGCGCGCAC	2508
Db	2461	GCTCGTATGCAAGCCCAAGGATTAAGGTGCTGTCTGTAACCCCTCGTCCGCGCGCAC	2520
Qy	2509	CTAGGTTTCGGGGGTATATGCTTAAGGCACATGGTATCGACCTAACATCAGAACCGG	2568
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Qy	2569	GTAAGGACCATCACACGGGTGCCCCATCACGTACTCCACTATGCGGAAGTTTCTTGCC	2628
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Qy	2629	GACGTTGGTTGCTCTGGGGCGCTATGACATCATATAATGTGATGAGTGCCACTCAACT	2688
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Qy	2749	CGACTCGTCTGTGCGCACCGCTAGCGCTCCGGATCGGTACCGTGCACATCAAAAC	2808
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Qy	2809	ATCAGAGGTGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCGAAAGCCATCCCC	2868
Db	2821	ATCAGAGGTGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCGAAAGCCATCCCC	2880
Qy	2869	ATCGAGCACTAAGGGGGGAGGCACTTCTCTGCCATTCCTCAAGAGAAATGTGAT	2928
Db	2881	ATCGAGCACTAAGGGGGGAGGCACTTCTCTGCCATTCCTCAAGAGAAATGTGAT	2940
Qy	2929	GAGCTCGCCCGAAGCTGTCCGSCCTCGACTCAATGCTGTAGCATATACCGGGGCTT	2988
Db	2941	GAGCTCGCCCGAAGCTGTCCGSCCTCGACTCAATGCTGTAGCATATACCGGGGCTT	3000

QY	2989	GATGATATCCGTCATACCAACTAGCGGAGACGCTCATTTGCTAGCAACGGACGCTCTAATG	3048
DB	3001	GATGTATCCGTATACCAACTAGCGGAGACGCTCATTTGCTGTCGACGAGCTCTAATG	3060
QY	3049	ACGGCGCTTTACCGGCGATTTCCAGTCACTAGTGATCGACTGCAATATCATGTCACCCAGACA	3108
DB	3061	ACGGCGCTTTACCGGCGATTTCCAGTCACTAGTGATCGACTGCAATATCATGTCACCCAGACA	3120
QY	3109	GTTCGACTTCAGCCTGGAACCCGACCTTCCACCATTCAGACGACGACCGTGCACACAGACGCG	3168
DB	3121	GTTCGACTTCAGCCTGGAACCCGACCTTCCACCATTCAGACGACGACCGTGCACACAGACGCG	3180
QY	3169	GTGTCACTCTCCAGCGCGGAGGAGGACTGTGTAGGGGCGAGGATGGGCATTTACAGTGT	3228
DB	3181	GTGTCACTCTCCAGCGCGGAGGAGGACTGTGTAGGGGCGAGGATGGGCATTTACAGTGT	3240
QY	3229	GTGACTCCAGAGAAACGGCCCTCCGGGCAATGTTGCAATTCCTCGGTTCTGTGCGAGTGCTAT	3288
DB	3241	GTGACTCCAGAGAAACGGCCCTCCGGGCAATGTTGCAATTCCTCGGTTCTGTGCGAGTGCTAT	3300
QY	3289	GACCGGGCTGTGCTTGCTTGCTAGAGCTCACGCCGCCGAGAGACCTCAGTTAGGTTGCGGGCT	3348
DB	3301	GACCGGGCTGTGCTTGCTTGCTAGAGCTCACGCCGCCGAGAGACCTCAGTTAGGTTGCGGGCT	3360
QY	3349	TACTCTAAACACACAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTCGGAGAGCGCTC	3408
DB	3361	TACTCTAAACACACAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTCGGAGAGCGCTC	3420
QY	3409	TTTACAGGCTTACCACATAGACGCCCATTTCTTTGCCAGACTAAGCAGGCGAGGAGAC	3468
DB	3421	TTTACAGGCTTACCACATAGACGCCCATTTCTTTGCCAGACTAAGCAGGCGAGGAGAC	3480
QY	3469	AACTTCCCTTACCTGTGTAGCATACGAGCTACCGTGTGCCAGGCTCAGGCTCCACCT	3528
DB	3481	AACTTCCCTTACCTGTGTAGCATACGAGCTACCGTGTGCCAGGCTCAGGCTCCACCT	3540
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DB	3601	ACGCCCTGCTGTATAGGCTGGGAGCGGTTCAAACGAGGTTACTACCAACACACCCCATATA	3660
QY	3649	ACCAAAATACATCATGGCATGCATGTCGGCTGCACCTCGAGGTCGTACAGGACCTGGTG	3708
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RESULT 3
US-09-539-601-22
; Sequence 22, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/5.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:

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; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture-adapted clone no. 5.1
; FEATURE:
; NAME/KEY: 5'UTR
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Query Match          99.4%; Score 7943; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7974; Conservative 0; Mismatches 15; Indels 12; Gaps 1;

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RESULT 4
US-09-539-601-16
; Sequence 16, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct 1389/NS3-3'/9-13F
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS

Mon Aug 16 09:32:31 2004

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; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural protein NS3-5B;
; OTHER INFORMATION: carries cell culture-adaptive mutations from clone
; OTHER INFORMATION: 9-13F
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)
; US-09-539-601-16

Query Match 99.4%; Score 7941.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;

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Query Match 99.3%; Score 7935; DB 4; Length 8001;
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Db 2941 GAGTCTGCGCGAAGCTGTCGCGCTCGGACTCAATGCTGTAGCATATTTACCGGGCCTT 3000
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Db 3061 ACGGGCTTTTACCGGCAATTTCCGACTCAGTGTGACTGCAATACATGTGTACCCAGACA 3120
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QY 3949 CAAGCGGAGTGTGCTTCCGTTGGAAATCCAAAGTGTGAGTGTGCTGCAACACGACCAAG 4008
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QY 4009 GCGAGCATATGTGGAATTTTCAATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTG 4068
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Db 4081 CCTGCAACCCCGGATAGCATCTGATGCAATTCAGGCTCTATCAGAGCCCGCTC 4140

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Db	4141	ACCACCCAAATATACCTCTCTGTTTAAATCTCTGGGGGATGGTGGCCGCCCAACTTGTCT	4200
Qy	4189	CCTCCACGCGCTCTCTCTGCTTTTCGTAGGCGCCGGCATCGCTGGAGCGGCTGTGGCAGC	4248
Db	4201	CCTCCACGCGTCTCTCTCTGCTTTTCGTAGGCGCCGGCATCGCTGGAGCGGCTGTGGCAGC	4260
Qy	4249	ATAGGCTTGGGAAGTGTCTGTGGATATTTTGGCAGGTTATCGACGAGGGTGGCAGGC	4308
Db	4261	ATAGGCTTGGGAAGTGTCTGTGGATATTTTGGCAGGTTATCGACGAGGGTGGCAGGC	4320
Qy	4309	GGCTCTCGTGGCTTTTAAAGTTCATGAGCGGCGAGATGCCCTCCACCGAGGACCTTGGCTAAC	4368
Db	4321	GGCTCTCGTGGCTTTTAAAGTTCATGAGCGGCGAGTGTCCCTCCACCGAGGACCTTGGTTAAC	4380
Qy	4369	CTACTCCCTGCTATCTCTCCCTGGGCGCCCTAGTCTGGGGTGTGTGGCGAGCGATTA	4428
Db	4381	CTACTCCCTGCTATCTCTCCCTGGGCGCCCTAGTCTGGGGTGTGTGGCGAGCGATTA	4440
Qy	4429	CTGGTCTGGCAGCTGGGCCCAAGGAGGGGGCTGTGCAAGTGGATGAACCGCTCATAGCG	4488
Db	4441	CTGGTCTGGCAGCTGGGGCCCAAGGAGGGGGCTGTGCAAGTGGATGAACCGCTCATAGCG	4500
Qy	4489	TTTCGCTTCGGGGGTAAACCAAGTCTCTCCCAACGCACTATGTGCTGAGAGCGAGCTGCA	4548
Db	4501	TTTCGCTTCGGGGGTAAACCAAGTCTCTCCCAACGCACTATGTGCTGAGAGCGAGCTGCA	4560
Qy	4549	GCACTGTCTACTCAGATCCTCTCTAGTCTTACCATCACTACAGCTGCTGAAGAGCTTTCAC	4608
Db	4561	GCACGAGTCACTCAGATCCTCTCTAGTCTTACCATCACTACAGCTGCTGAAGAGCTTTCAC	4620
Qy	4609	CAGTGGATCAACGAGGACTGTCTCCACGCGCATGCTCCGGCTCTGGCTAAGAGATGTTTGG	4668
Db	4621	CAGTGGATCAACGAGGACTGTCTCCACGCGCATGCTCCGGCTCTGGCTAAGAGATGTTTGG	4680
Qy	4669	GATTGGATATGACCGGTGTGACTGAATTTAAGACTCTGGCTCCAGTCCAGCTCTTGCGG	4728
Db	4681	GATTGGATATGACCGGTGTGACTGAATTTAAGACTCTGGCTCCAGTCCAGCTCTTGCGG	4740
Qy	4729	CGATTTCCGGGAGTCCCTTCTCTCATGTCAACCTGGGTACAAGGGAGTCTGGCGGGG	4788
Db	4741	CGATTTCCGGGAGTCCCTTCTCTCATGTCAACCTGGGTACAAGGGAGTCTGGCGGGG	4800
Qy	4789	GACGGCATCATGCAAAACCACTGCCAATGTGAGCACAGATCACCGGACATGTGAAAAA	4848
Db	4801	GACGGCATCATGCAAAACCACTGCCAATGTGAGCACAGATCACCGGACATGTGAAAAA	4860
Qy	4849	GGTTCCATGAGGATCGTGGGGCTAGGACCTGTAGTAAACGTGTCATGGAACATTCCTCC	4908
Db	4861	GGTTCCATGAGGATCGTGGGGCTAGGACCTGTAGTAAACGTGTCATGGAACATTCCTCC	4920
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Db	4921	ATTAAACGCGTACACCAAGCGCCCTCTGACGCCCTCCCGCGCCCAAAATTTCTAGGGG	4980
Qy	4969	CTGTGGGGGTGCTGCTGAGGATGATGGAGGTTACCGGGTGGGGATTTCCACTAC	5028
Db	4981	CTGTGGGGGTGCTGCTGAGGATGATGGAGGTTACCGGGTGGGGATTTCCACTAC	5040
Qy	5029	GTACAGGGCATACCACTGACAAACGTAAAGTGGCCCTGTCAAGTTCCGGCCCGCAATTC	5088
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Db	6361	TGGAAGGACTTGCTGGAAAGACACTGAGACACCAATTGACACCACTCATGCGCAAAAAT	6420
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Db	6481	CCAGATTTGGGGTTCGTCGTGCGAGAGAAATGCGCCTTTACGATGTGTCTCCACGCTC	6540
Qy	6529	CCTCAGGCGGTGATGGGCTCTTCATACGGAATCCAAATCTCTCTGACAGCGGGTCTGAG	6588
Db	6541	CCTCAGGCGGTGATGGGCTCTTCATACGGAATCCAAATCTCTCTGACAGCGGGTCTGAG	6600
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Qy	6769	GGGGGCCCCCTGACTAAATTTCTAAAGGCGAGAACTCGGCTATCGCGGTGCCCGCGAGC	6828
Db	6781	GGGGGCCCCCTGACTAAATTTCTAAAGGCGAGAACTCGGCTATCGCGGTGCCCGCGAGC	6840
Qy	6829	GGTCTACTGACGACAGCTCGGTGTAATACCTTCATCTGTTAAGGCGGCTGCGGCC	6888
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Qy	6889	TGTCGAGCTCGGAAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTTGTGCTT	6948
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Qy	6949	ATCTGTGAAAGCGGGGACCCCAAGAGGACGAGCGGAGCCTACGGGCTTTCACGGAGGCT	7008
Db	6961	ATCTGTGAAAGCGGGGACCCCAAGAGGACGAGCGGAGCCTACGGGCTTTCACGGAGGCT	7020
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Db	7021	ATGACTAGATACTCTGCCCCCTGGGACCGCGGCCAAACCCAGAAATCGACTTTGAGTTG	7080
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Db	7081	ATAACATCATGCTCCCTCCAAATGTTGAGTCGCGCACGATGTCATCTGGCAAAAGGTTGAC	7140
Qy	7129	TATCTCACCGGTGAACCCACACCCCTTTGCGGGCTGCGGTGGAGACAGCTAGACAC	7188
Db	7141	TATCTCACCGGTGAACCCACACCCCTTTGCGGGCTGCGGTGGAGACAGCTAGACAC	7200
Qy	7189	ACTCCAGTCAATTCCTGGCTAGGCAATCATCATGTATGCGGCCACCTTGTGGGCAAGG	7248
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Qy	7249	ATGATCTGATGACTCATTTCTTCTCCACTTCTAGCTCAGGAACTTGTGAAAAGCC	7308
Db	7261	ATGATCTGATGACTCATTTCTTCTCACTCTTCTAGCTCAGGAACTTGTGAAAAGCC	7320
Qy	7309	CTAGATTGTGAGATCTACGGGGCTGTATCTCCATTGAGCCACTTCACTCAGATC	7368
Db	7321	CTAGATTGTGAGATCTACGGGGCTGTATCTCCATTGAGCCACTTCACTCAGATC	7380
Qy	7369	ATTCAAGGACTCCATGGCTTAGGCAATTTCTCATCTAGTTACTCTCCAGGTGAGATC	7428

Db	7381	ATTCAAAGACTCCATGGCGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATC	7440
Qy	7429	AATAGGGTGGCTTCATGGCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTCGAGACAT	7488
Db	7441	AATAGGGTGGCTTCATGGCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTCGAGACAT	7500
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Db	7801	CCATCCTGTTTTTTTCCCTTT	7860
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Qy	7909	CCTAGTCAAGGCTAGCTGTGAAGGTCCTGTAGCCGCTTGAAGTGCAGAGAGTGTGTATAC	7968
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US-09-539-601-4			
; Sequence 4, Application US/09539601C			
; Patent No. 6630343			
; GENERAL INFORMATION:			
; APPLICANT: Bartenschlager, Ralf FW			
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System			
; FILE REFERENCE: all sequences			
; CURRENT APPLICATION NUMBER: US/09/539,601C			
; CURRENT FILING DATE: 2001-08-30			
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY			
; EARLIER FILING DATE: 1999-04-03			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 4			
; LENGTH: 8637			
; TYPE: DNA			
; ORGANISM: Hepatitis C virus			
; FEATURE:			
; NAME/KEY: 5'UTR			
; LOCATION: (1)..(341)			
; OTHER INFORMATION: construct I377/NS2-3'/wt			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (342)..(1181)			
; OTHER INFORMATION: HCV core-neomycin phosphotransferase fusion			
; FEATURE:			
; NAME/KEY: RBS			
; LOCATION: (1190)..(1900)			

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QY	3313	CTCAGCCGCGCCGAGACCTCAGTTAGTTGGGGCTTACCTAAACACACGAGGTTGCCC	3372	Db	5041	GGCGCCCTAGTCGTGGGGTCTGTCGCGAGGATCTGCGTCGCGACGTCGGGCGCCAGGG	5100
Db	3361	CTCAGCCGCGCCGAGACCTCAGTTAGTTGGGGCTTACCTAAACACACGAGGTTGCCC	4020	QY	4453	GAGGGGGTGTGAGTGAGTGAACCGGCTGATAGGTTGCTTCCGCGGGTAAACACGTC	4512
QY	3373	GTCTGCCAGGACCATCTGGAGTCTGGGAGAGCGTCTTTTACGAGGCTCACCACATAGAC	3432	Db	5101	GAGGGGGTGTGAGTGAGTGAACCGGCTGATAGGTTGCTTCCGCGGGTAAACACGTC	5160
Db	4021	GTCTGCCAGGACCATCTGGAGTCTGGGAGAGCGTCTTTTACGAGGCTCACCACATAGAC	4080	QY	4513	TCCCCACGCACTATGTGCTGAGAGCGACGCTGCAGCACGTCCTCACTCAGATCCTCTCT	4572
QY	3433	GCCATTCTTCTCCAGACTAAGCAGGACGAGAGCAACTTCCCTCACTCTGGTAGCATAC	3492	Db	5161	TCCCCACGCACTATGTGCTGAGAGCGACGCTGCAGCACGTCCTCACTCAGATCCTCTCT	5220
Db	4081	GCCATTCTTCTCCAGACTAAGCAGGACGAGAGCAACTTCCCTCACTCTGGTAGCATAC	4140	QY	4573	AGTCTTACCATCACTAGCTCTGAAGAGGCTTCAACAGTGAGTCAACGAGGACTGTCTTC	4632
QY	3493	CAGGCTACGGTGTGCGCAGGCTCAGGCTCAGCTCCTCATGCTGGGACCAATGTGGAG	3552	Db	5221	AGTCTTACCATCACTAGCTCTGAAGAGGCTTCAACAGTGAGTCAACGAGGACTGTCTTC	5280
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QY	3793	GGAAGCCGCGCATCATTTCCGACAGGAGTCTTTTACCAGGAGTTCATGAGTGGAA	3852	Db	5521	AGGACCTGTAGTAAACACAGTGGCATGGAACATTTCCCATTTAAACGCGTACACCGGCCCC	5580
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RESULT 7
US-09-539-601-13
; Sequence 13, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8649
; TYPE: DNA
; ORGANISM: Hepatitis C virus
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; NAME/KEY: 5'UTR
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; NAME/KEY: CDS
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; OTHER INFORMATION: hepatitis C virus NS2 - 5B
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; NAME/KEY: 3'UTR
; LOCATION: (8419)..(8649)
; PUBLICATION INFORMATION:
; AUTHORS: Lohmann, Volker
; AUTHORS: Krner, Frank
; AUTHORS: Koch, Jan-Oliver
; AUTHORS: Herian, Ulrike
; AUTHORS: Theilmann, Lorenz
; AUTHORS: Bartenschlager, Ralf
; TITLE: Replication of subgenomic hepatitis c virus RNAs in a
; TITLE: hepatoma cell line
; JOURNAL: Science
; VOLUME: 285
; PAGES: 110-113
; DATE: 1999-07-02
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US-09-539-601-13

Query Match 91.4%; Score 7302.6; DB 4; Length 8649;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 660; Gaps 2;

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DB 2461 CTCGCGCTTATTAAGGCTTACTCCCAACAGACGCGAGGCTTACTTGGCTGCATCATCACT 2520
QY 1861 AGCTCTACAGCGCGGACAGGAAACAGGTCGAGGGGAGGTCCAGGTGTCTCCACCGCA 1920
DB 2521 AGCTCTACAGCGCGGACAGGAAACAGGTCGAGGGGAGGTCCAGGTGTCTCCACCGCA 2580
QY 1921 ACACAATCTTCTGGCGACTCTCGTCAATGGGCTGTGTGGACTGTCTATCATGTGTC 1980
DB 2581 ACACAATCTTCTGGCGACTCTCGTCAATGGGCTGTGTGGACTGTCTATCATGTGTC 2640
QY 1981 GGCTCAAGACCTTGGCGGCTTCCGCGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
DB 2641 GGCTCAAGACCTTGGCGGCTTCCGCGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2700
QY 2041 CAGGACTCTCGTGGTGGCAAGCGCCCCCGGGGCGGTCTCTTGACACCATGCACTGC 2100
DB 2701 CAGGACTCTCGTGGTGGCAAGCGCCCCCGGGGCGGTCTCTTGACACCATGCACTGC 2760
QY 2101 GGCACTCGGACTTCTTACTTGTGTCAGGACATGCGGATGTCTATCCGGTGGCGCGCG 2160
DB 2761 GGCACTCGGACTTCTTACTTGTGTCAGGACATGCGGATGTCTATCCGGTGGCGCGCG 2820
QY 2161 GGCGACAGGAGGAGCTTCTCTCCCGAGGCGCTCTCTTCTTGAAGGCTCTTTCG 2220
DB 2821 GGCGACAGGAGGAGCTTCTCTCTCCCGAGGCGCTCTCTTCTTGAAGGCTCTTTCG 2880
QY 2221 GSCGTCTCACTGTCTTGGCGGCGCTGTGGGCGATCTTTCGGGCTGCGGCTGC 2280
DB 2881 GSCGTCTCACTGTCTTGGCGGCGCTGTGGGCGATCTTTCGGGCTGCGGCTGC 2940
QY 2281 ACCGAGGGGTTGCGAAGCGGTGACTTTGTACCGTCTGAGTCTATGGAACCACTATG 2340
DB 2941 ACCGAGGGGTTGCGAAGCGGTGACTTTGTACCGTCTGAGTCTATGGAACCACTATG 3000
QY 2341 CGGTCCCCGCTTCTACGAGCAACTCTGCTCCCTCGGCGGTAACCGGACATTCAGGTT 2400
DB 3001 CGGTCCCCGCTTCTACGAGCAACTCTGCTCCCTCGGCGGTAACCGGACATTCAGGTT 3060
QY 2401 GGCCTACTACAGCCCTTCTGCTAGCGCAAGACACTTAAGTGCCTGCGCTGCTATGCA 2460
DB 3061 GGCCTACTACAGCCCTTCTGCTAGCGCAAGACACTTAAGTGCCTGCGCTGCTATGCA 3120
QY 2461 GCGCAAGGTTATAGGTTGCTTCTGTAACCGCTCGGCGGCAACCCCTAGGTTTCGGG 2520
DB 3121 GCGCAAGGTTATAGGTTGCTTCTGTAACCGCTCGGCGGCAACCCCTAGGTTTCGGG 3180
QY 2521 GGTATATGTCTAAGGCAATGGTATCGACCCCTAATCATCAGAACCGGGGTAGGACCATC 2580

QY	4741	GTCCCTCTTCTTCTCATGTCAACGTGGGTACAAAGCGAGTCTGGCGGGCGACCGCATCATG	4801
DB	5401	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGCGACCGCATCATG	5460
QY	4801	CAAAACCACTCGCCATGTGGAGCAAGATCACCGGACATGTGAAAAAGGTTCCATGAGG	4860
DB	5461	CAAAACCACTCGCCATGTGGAGCAAGATCACCGGACATGTGAAAAAGGTTCCATGAGG	5520
QY	4861	ATCTGTGGGCCCTAGGACTGTAGTAAACAGTGGGCATGGAACAATCCCTCCATTAACGGGTAC	4920
DB	5521	ATCTGTGGGCCCTAGGACTGTAGTAAACAGTGGGCATGGAACAATCCCTCCATTAACGGGTAC	5580
QY	4921	ACCAAGGGCCCTCGACGCCCTCCCGCGCGCAAAATTAATCTAGGGCGCTGTGGCGGGTG	4980
DB	5581	ACCAAGGGCCCTCGACGCCCTCCCGCGCGCAAAATTAATCTAGGGCGCTGTGGCGGGTG	5640
QY	4981	GCTCTGAGGAGTACGTGGAGTTACGCGGTGGGGATTTCCACTACGTGACGGGCATG	5040
DB	5641	GCTCTGAGGAGTACGTGGAGTTACGCGGTGGGGATTTCCACTACGTGACGGGCATG	5700
QY	5041	ACCACTCACAACTGTAAGTCCCGTGTACGGTTCGGCCCCCGAAATCTTTCACAGAAGTG	5100
DB	5701	ACCACTCACAACTGTAAGTCCCGTGTGTACGGTTCGGCCCCCGAAATCTTTCACAGAAGTG	5760
QY	5101	GATGGGTGGGGTTGCACAGTACGCTCCAGCGTGCAAACCCCTCTACGGGAGGAGTTC	5160
DB	5761	GATGGGTGGGGTTGCACAGTACGCTCCAGCGTGCAAACCCCTCTACGGGAGGAGTTC	5820
QY	5161	ACATTCCTGTGCGGCTCAATCAATACCTGTTGGGTACAGCTCCCATGCGAGCCCGAA	5220
DB	5821	ACATTCCTGTGCGGCTCAATCAATACCTGTTGGGTACAGCTCCCATGCGAGCCCGAA	5880
QY	5221	CCGAGCTAGCAGTGCTCACTTCAGTCTCACCGACCCCTCCCAATTAACGCGAGAGCG	5280
DB	5881	CCGAGCTAGCAGTGCTCACTTCAGTCTCACCGACCCCTCCCAATTAACGCGAGAGCG	5940
QY	5281	GCTAAGCTAGGCTGGCCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
DB	5941	GCTAAGCTAGGCTGGCCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAG	6000
QY	5341	CTGTCTGGGCTTCTTTGAAGGCAACATGACATPACCCGTCACTCCCGGACGCTGAC	5400
DB	6001	CTGTCTGGGCTTCTTTGAAGGCAACATGACATPACCCGTCACTCCCGGACGCTGAC	6060
QY	5401	CTCATTCAGGCCAACTCTGTGGCGGAGGAGTGGCGGGAAATCAACCCCGTGGAG	5460
DB	6061	CTCATTCAGGCCAACTCTGTGGCGGAGGAGTGGCGGGAAATCAACCCCGTGGAG	6120
QY	5461	TCAGAAAAAAGGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCAAAGCGGAGGAGATCAG	5520
DB	6121	TCAGAAAAAAGGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCAAAGCGGAGGAGATCAG	6180
QY	5521	AGGGAAGTATCGTTCCGGGGAGATCTCTGGGAGGTCCAGAAAATTCCTTCGAGCGATG	5580
DB	6181	AGGGAAGTATCGTTCCGGGGAGATCTCTGGGAGGTCCAGAAAATTCCTTCGAGCGATG	6240
QY	5581	CCCATATGGGCACGCCCGGATTAACACCTCCACTTTAGAGTCTCTGGAAGAACCCCGAC	5640
DB	6241	CCCATATGGGCACGCCCGGATTAACACCTCCACTTTAGAGTCTCTGGAAGAACCCCGAC	6300
QY	5641	TACGTCCTCCAGTGGTACACGGGTGTCCATTTCCGCGCTGCCAAGGCCCTCCCATACCA	5700
DB	6301	TACGTCCTCCAGTGGTACACGGGTGTCCATTTCCGCGCTGCCAAGGCCCTCCCATACCA	6360
QY	5701	CCTCCACGAGGAAGGAGCGTTGTCTGTTCAGAAATCTACCGTGTCTTCTGCCTTGCG	5760
DB	6361	CCTCCACGAGGAAGGAGCGTTGTCTGTTCAGAAATCTACCGTGTCTTCTGCCTTGCG	6420
QY	5761	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAAATCGTGGCGGTTCGACAGCGGCACGGCA	5820
DB	6421	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAAATCGTGGCGGTTCGACAGCGGCACGGCA	6480

QY	5821	ACGGCTCTCTCTGACCAAGCCCTTCGACGACGCGACGCGGATCCGAGCTTGAGTTCGTAC	5881
DB	6481	ACGGCTCTCTCTCTGACCAAGCCCTTCGACGACGCGACGCGGATCCGAGCTTGAGTTCGTAC	6540
QY	5881	TCCTCATGCCCCCTTTGAGGGGGAGCGCGGGATTCGGATCTCAGGACGGGTCTTTGG	5940
DB	6541	TCCTCATGCCCCCTTTGAGGGGGAGCGCGGGATCCGATCTCTACGACGGGTCTTTGG	6600
QY	5941	TCTACCGTAAGCGAGGAGCTAGTGAGGACGTCTCTGCTGCTGATGTCCTACACATGG	6000
DB	6601	TCTACCGTAAGCGAGGAGCTAGTGAGGACGTCTCTGCTGCTGATGTCCTACACATGG	6660
QY	6001	ACAGCGCCCTGATACAGCCCATCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTG	6060
DB	6661	ACAGCGCCCTGATACAGCCATCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTG	6720
QY	6061	AGCAACTCTTTGCTTCGGTCACCAAACTTTGGTCTATGCTACACATCTCGACGGCAAGC	6120
DB	6721	AGCAACTCTTTGCTTCGGTCACCAAACTTTGGTCTATGCTACACATCTCGACGGCAAGC	6780
QY	6121	CTGCGGCAGAAAGAGTCACTTTGACAGACTGCAAGTCTCTGACGACCACTACCGGAC	6180
DB	6781	CTGCGGCAGAGAGAGTCACTTTGACAGACTGCAAGTCTCTGACGACCACTACCGGAC	6840
QY	6181	GTGCTCAAGGAGATGAAGGCGAAGGCGTCCACAGTTAAAGCTTAAAGCTTAAAGCTGAG	6240
DB	6841	GTGCTCAAGGAGATGAAGGCGAAGGCGTCCACAGTTAAAGCTTAAAGCTTAAAGCTGAG	6900
QY	6241	GAAGCTGTAAAGCTGACGCGCCCACTTCGGCCAGATCTTAAATTTGGCTATGCGGCAAG	6300
DB	6901	GAAGCTGTAAAGCTGACGCGCCCACTTCGGCCAGATCTTAAATTTGGCTATGCGGCAAG	6960
QY	6301	GACGTCGCGAACCTTATCCAGCAAGCGCGTTAAACCATCGCTCCGCTGCGGAGCACTTG	6360
DB	6961	GACGTCGCGAACCTTATCCAGCAAGCGCGTTAAACCATCGCTCCGCTGCGGAGCACTTG	7020
QY	6361	CTGGAAGACACTGAGACACAAATTGACACCAACATCATGCGCAAAATAGAGTTTCTGC	6420
DB	7021	CTGGAAGACACTGAGACACAAATTGACACCAACATCATGCGCAAAATAGAGTTTCTGC	7080
QY	6421	GTCCAAACGAGAGGGGGCGCCAGCCAGCTGCGCTTATCGTATTTCCAGATTGGGG	6480
DB	7081	GTCCAAACGAGAGGGGGCGCCAGCCAGCTGCGCTTATCGTATTTCCAGATTGGGG	7140
QY	6481	GTTCTGTGTGCGAGAAATGGCCCTTTACGATGTGGTCTCCACCTCCCTCAGCGCGTG	6540
DB	7141	GTTCTGTGTGCGAGAAATGGCCCTTTACGATGTGGTCTCCACCTCCCTCAGCGCGTG	7200
QY	6541	ATGGGCTCTTCATACGGATTTCAAATCTCTCTGGACAGCGGTTCGAGTTCTCGTGAAT	6600
DB	7201	ATGGGCTCTTCATACGGATTTCAAATCTCTCTGGACAGCGGTTCGAGTTCTCGTGAAT	7260
QY	6601	GCTTGAAGACGAGAAATGCCCTATGGCTTCGATATGACACCCGCTGTTTTGACTCA	6660
DB	7261	GCTTGAAGACGAGAAATGCCCTATGGCTTCGATATGACACCCGCTGTTTTGACTCA	7320
QY	6661	ACGGTCACTGAGAAATGACATCCGCTGTGAGGAGTCAAATCTACCAATGTGTGACTTGCC	6720
DB	7321	ACGGTCACTGAGAAATGACATCCGCTGTGAGGAGTCAAATCTACCAATGTGTGACTTGCC	7380
QY	6721	CCGGAAGCAGACAGGCCATAGGTGCTCAGAGCGGCTTTATCATCGGGGGCCCCCTG	6780
DB	7381	CCGGAAGCAGACAGGCCATAGGTGCTCAGAGCGGCTTTATCATCGGGGGCCCCCTG	7440
QY	6781	ACTAATTTAAAGGCGAGAACTGCGGCTATCGCCGTCGCGGCGAGCGGTGTACTGACG	6840
DB	7441	ACTAATTTAAAGGCGAGAACTGCGGCTATCGCCGTCGCGGCGAGCGGTGTACTGACG	7500
QY	6841	ACCAGTCGGTAAATACCTCATAGTTTAAAGGCGCTGCGGCTGTCGAGCTGCG	6900
DB	7501	ACCAGTCGGTAAATACCTCATAGTTTAAAGGCGCTGCGGCTGTCGAGCTGCG	7560
QY	6901	AGGCTCCAGATGACAGATGCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960

7561	DB	 AAGCTCCAGGACTGCAGATGCTCGTATGCGGAGACGACCTTGTCGTTATCTGTGAAGC	7620
6961	QY	CGGGGACCCAAAGAGGACGAGCGAGCCTACGGCCCTTCAGGGAGGCTAGCTAGATAC	7020
7621	DB	CGGGGACCCAAAGAGGACGAGCGAGCCTACGGCCCTTCAGGGAGGCTAGCTAGATAC	7680
7021	QY	TCTGCCCCCTGGGGACCCGCCAAACCGAATACGACTTGGAGTTGATAAATCATGCG	7080
7681	DB	TCTGCCCCCTGGGGACCCGCCAAACCGAATACGACTTGGAGTTGATAAATCATGCG	7740
7081	QY	TCCTCCAATGTGTAGTCGCGACGATGATCTTGCAAAAGGGTGTACTATCTCACCGGT	7140
7741	DB	TCCTCCAATGTGTAGTCGCGACGATGATCTTGCAAAAGGGTGTACTATCTCACCGGT	7800
7141	QY	GACCCACACGCCCTTTCGCGGGCTGCGTGGGAGACGCTAGACACATCCAGTCAAT	7200
7801	DB	GACCCACACGCCCTTTCGCGGGCTGCGTGGGAGACGCTAGACACATCCAGTCAAT	7860
7201	QY	TCCTGGCTAGGCAACATCATCATGTATGCGCCACTTGTGGGCAAGGATGATCCTGATG	7260
7861	DB	TCCTGGCTAGGCAACATCATCATGTATGCGCCACTTGTGGGCAAGGATGATCCTGATG	7920
7261	QY	ACTCATTTCTTCTCCATCCTTCTAGCTCAGGAACTTGAAAAAGCCTAGATTGTGAG	7320
7921	DB	ACTCATTTCTTCTCCATCCTTCTAGCTCAGGAACTTGAAAAAGCCTAGATTGTGAG	7980
7321	QY	ATCTAGGGGCTGTTTATCTCCATGTAGGCCATTTGACTTACCTCAGATCATTTCAAGGCTC	7380
7981	DB	ATCTAGGGGCTGTTTATCTCCATGTAGGCCATTTGACTTACCTCAGATCATTTCAAGGCTC	8040
7381	QY	CATGGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
8041	DB	CATGGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	8100
7441	QY	TCATGGCTCAGGAAACTTGGGGTACGCCCTTTCGGAGCTCGGAGCATCGGGCCAGAGT	7500
8101	DB	TCATGGCTCAGGAAACTTGGGGTACGCCCTTTCGGAGCTCGGAGCATCGGGCCAGAGT	8160
7501	QY	GTCCGGCTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
8161	DB	GTCCGGCTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	8220
7561	QY	AACCTGGCGTAGAGGACCAAGCTCAAACTCACCTCCAAATCCCGCTGCGTCCAGTTGGAT	7620
8221	DB	AACCTGGCGTAGAGGACCAAGCTCAAACTCACCTCCAAATCCCGCTGCGTCCAGTTGGAT	8280
7621	QY	TTATCCAGCTTGGTTTGGTTAGCGGGGGAGACATATATCACAGCTGTCTCGT	7680
8281	DB	TTATCCAGCTTGGTTTGGTTAGCGGGGGAGACATATATCACAGCTGTCTCGT	8340
7681	QY	GCGCGACCCCGCTGGTTTCATGTGGTCTACTCTACTTCTGTAGGGCTAGGCATCTAT	7740
8341	DB	GCGCGACCCCGCTGGTTTCATGTGGTCTACTCTACTTCTGTAGGGCTAGGCATCTAT	8400
7741	QY	CTACTCCCAACCGATCAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTTT	7800
8401	DB	CTACTCCCAACCGATCAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTTT	8460
7801	QY	TTTTCCCTTCTCCTTTT	7860
8461	DB	TTTTCCCTTCTCCTTTT	8520
7861	QY	TTTTTTCCTTACGCGC	7920
8521	DB	TTTTTTCCTTACGCGC	8580
7921	QY	TAGCTGTGAAAGGTCGCTGAGCCGCTTGACTGCAGAGAGTGTGATCTGGCCTCTCTGC	7980
8581	DB	TAGCTGTGAAAGGTCGCTGAGCCGCTTGACTGCAGAGAGTGTGATCTGGCCTCTCTGC	8640
7981	QY	AGATCAAGT	7989

QY	2160	GGGCGACAGCAGGGGAGCCTACTCTCCCGAGGCCGCTCTCCTACTTTGAAGGGCTCTTC	2219
Db	5247	GGGCGACAGCAGGGGAGCCTACTCTCCCGAGGCCGCTCTCCTACTTTGAAGGGCTCTTC	5306
QY	2220	GGGCGGTCCACTGCTCTCCCGCTCGGGGACGCTGTGGGCATCTTTTCGGGCTGCCGTGTG	2279
Db	5307	GGGCGGTCCACTGCTCTCCCGCTCGGGGACGCTGTGGGCATCTTTTCGGGCTGCCGTGTG	5366
QY	2280	CACCGAGGGGTTCGGAAGGCGGTGGACTTTGTATCCCGCTCAGTCTATGGAAAACACTAT	2339
Db	5367	CACCGAGGGGTTCGGAAGGCGGTGGACTTTGTATCCCGCTCAGTCTATGGAAAACACTAT	5426
QY	2340	CGGCTCCCGGTCTTTCACGGCAAACTCGTCCCGCTCGGCCCTACCGCAGACATTCAGGT	2399
Db	5427	CGGCTCCCGGTCTTTCACGGCAAACTCGTCCCGCTCGGCCCTACCGCAGACATTCAGGT	5486
QY	2400	GGCCCATCTACACGCCCTCTCTGTAGCGGCAAGACACTAAGGTGCCGTGCTATGC	2459
Db	5487	GGCCCATCTACACGCCCTCTCTGTAGCGGCAAGACACTAAGGTGCCGTGCTATGC	5546
QY	2460	AGCCCAAGGGTATAAGGTGCTTGTCTGAACCCGCTCGGCTCGGCCACCTTAGTTCGG	2519
Db	5547	AGCCCAAGGGTATAAGGTGCTTGTCTGAACCCGCTCGGCTCGGCCACCTTAGTTCGG	5606
QY	2520	GGCGTATATGTCTAAGGCACATGTTATCGACCCCTAAACATCAGAACCGGGTAAAGACCAT	2579
Db	5607	GGCGTATATGTCTAAGGCACATGTTATCGACCCCTAAACATCAGAACCGGGTAAAGACCAT	5666
QY	2580	CACACGGGTGCCCCATCAGTACTCCACTATGGCAAGTTTCTGCCGACGGTGGTTG	2639
Db	5667	CACACGGGTGCCCCATCAGTACTCCACTATGGCAAGTTTCTGCCGACGGTGGTTG	5726
QY	2640	CTCTGGGGGGCGCTATCAGATCATATATGTAGTGTGACCTCACTCACTGACCTCGACC	2699
Db	5727	CTCTGGGGGGCGCTATCAGATCATATATGTAGTGTGACCTCACTCACTGACCTCGACC	5786
QY	2700	TATCTGGGCATCGGCACAGTCTCTGGACCAAGGGGAGACGGCTGGAGCGGACCTCGTCTG	2759
Db	5787	TATCTGGGCATCGGCACAGTCTCTGGACCAAGGGGAGACGGCTGGAGCGGACCTCGTCTG	5846
QY	2760	GCTCGGCACCGCTACGGCTCGGGATCGGTCAACGTCGCCACATCCAAACATCAGGAGGT	2819
Db	5847	GCTCGGCACCGCTACGGCTCGGGATCGGTCAACGTCGCCACATCCAAACATCAGGAGGT	5906
QY	2820	GGCTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAGAGCCATCCCATCCAGACCAT	2879
Db	5907	GGCTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAGAGCCATCCCATCCAGACCAT	5966
QY	2880	CAGGGGGGAGGACCTCATTTTCTGCCATTCCTCAAGAGAAATGTGATGAGCTCGCCGC	2939
Db	5967	CAGGGGGGAGGACCTCATTTTCTGCCATTCCTCAAGAGAAATGTGATGAGCTCGCCGC	6026
QY	2940	GAAGCTGTCCGGCTCGGACTCAATCTGTAGCATATTAACGGGGCTTGATGATCCGT	2999
Db	6027	GAAGCTGTCCGGCTCGGACTCAATCTGTAGCATATTAACGGGGCTTGATGATCCGT	6086
QY	3000	CATACCAATAGCGGAGAGCTCATTTCTGTAGCAACGGAGCTCTAATCAGCGGCTTTAC	3059
Db	6087	CATACCAATAGCGGAGAGCTCATTTCTGTAGCAACGGAGCTCTAATCAGCGGCTTTAC	6146
QY	3060	CGGCGATTTGCACTCAGTGCATATCATGTGTCAACGACAGTGCATTTAC	3119
Db	6147	CGGCGATTTGCACTCAGTGCATATCATGTGTCAACGACAGTGCATTTAC	6206
QY	3120	CCTGGACCGGACTTACCATTTGAGACGACCGGTGCCAAGACGGGTGTACGCTC	3179
Db	6207	CCTGGACCGGACTTACCATTTGAGACGACCGGTGCCAAGACGGGTGTACGCTC	6266
QY	3180	GCAGCGGGGAGGACGACTGTGGGGGAGGATGGGCAATTTACAGTTTGTACTCCAGG	3239
Db	6267	GCAGCGGGGAGGACGACTGTGGGGGAGGATGGGCAATTTACAGTTTGTACTCCAGG	6326

QY	3240	AGAACGGCCCTCGGCGATGTTTGGATTCTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTG	3299
Db	6327	AGAACGGCCCTCGGCGATGTTTGGATTCTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTG	6386
QY	3300	TGCTTTGTTACAGCTCAGCGCCGCGAGACCTCTAGTTAGGTTTGGGGCTTACCTAAACAC	3359
Db	6387	TGCTTTGTTACAGCTCAGCGCCGCGAGACCTCTAGTTAGGTTTGGGGCTTACCTAAACAC	6446
QY	3360	ACCAGGGTTCGCCCTCTGCCAGGACCATCTCGAGTTCTGGGAGAGCCTTTTACAGGCT	3419
Db	6447	ACCAGGGTTCGCCCTCTGCCAGGACCATCTCGAGTTCTGGGAGAGCCTTTTACAGGCT	6506
QY	3420	CACCCATAGACGCCCATTTTCTTGTCTCCAGACTTAAGCAGCAGGAGACAACTTCCCTTA	3479
Db	6507	CACCCATAGACGCCCATTTTCTTGTCTCCAGACTTAAGCAGCAGGAGACAACTTCCCTTA	6566
QY	3480	CCTGGTAGCATACCAAGCTACGGTGTGGCCAGGCTCAGGCTCCACTCCATCGTGGGA	3539
Db	6567	CCTGGTAGCATACCAAGCTACGGTGTGGCCAGGCTCAGGCTCCACTCCATCGTGGGA	6626
QY	3540	CCAAATGTGAAGTGTCTCATACGGCTAAAGCCTTACGCTGACCGGGCCAAACCCCTGCT	3599
Db	6627	CCAAATGTGAAGTGTCTCATACGGCTTAAAGCCTTACGCTGACCGGGCCAAACCCCTGCT	6686
QY	3600	GTATAGGCTGGAGCCGTTCAAACAGAGGTTACTTACACACACCCCATTAACCAATACAT	3659
Db	6687	GTATAGGCTGGAGCCGTTCAAACAGAGGTTACTTACACACACCCCATTAACCAATACAT	6746
QY	3660	CATGGCATGATGTGGCTGACCTGGAGTGTCTACAGCAGCCTTGGGTGTGTAGGCGG	3719
Db	6747	CATGGCATGATGTGGCTGACCTGGAGTGTCTACAGCAGCCTTGGGTGTGTAGGCGG	6806
QY	3720	AGTCTTAGCAGCTCTGGCCGCGTATTGCTCTGACAAACAGGAGCGTGTCTATTGTGGCAG	3779
Db	6807	AGTCTTAGCAGCTCTGGCCGCGTATTGCTCTGACAAACAGGAGCGTGTCTATTGTGGCAG	6866
QY	3780	GATCATCTTGTCCGGAAGCGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGGAGTT	3839
Db	6867	GATCATCTTGTCCGGAAGCGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGGAGTT	6926
QY	3840	CGATGAGTGAAGAGTGGCGCTCACACCTTCTTACATCTGAACAGGGAATGAGCTCGC	3899
Db	6927	CGATGAGTGAAGAGTGGCGCTCACACCTTCTTACATCTGAACAGGGAATGAGCTCGC	6986
QY	3900	CGAACAAATTTCAAACAGAGGCAATCGGGTTGTCTGCAAAACAGCAGCAGGAGGCG	3959
Db	6987	CGAACAAATTTCAAACAGAGGCAATCGGGTTGTCTGCAAAACAGCAGCAGGAGGCG	7046
QY	3960	TGCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTTCGAAGCCCTTCTGGCGGAAGCATAT	4019
Db	7047	TGCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTTCGAAGCCCTTCTGGCGGAAGCATAT	7106
QY	4020	GTGGAATTTTCATCAGCGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGGCAACCC	4079
Db	7107	GTGGAATTTTCATCAGCGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGGCAACCC	7166
QY	4080	CGCGATAGCATCAGTGAAGCATTCAGCCTCTATCAGCAGCCGCTCACACCCCAACA	4139
Db	7167	CGCGATAGCATCAGTGAAGCATTCAGCCTCTATCAGCAGCCGCTCACACCCCAACA	7226
QY	4140	TACCCCTCTGTTTACATCTCTGGGGGATGGTGGCGGCCCAACTTGTCTTCCAGCGC	4199
Db	7227	TACCCCTCTGTTTACATCTCTGGGGGATGGTGGCGGCCCAACTTGTCTTCCAGCGC	7286
QY	4200	TGCTTCTGCTTTCGTAGCGCGCATCGCTGGAGCGGCTGTGGCAGATAGGCTTGG	4259
Db	7287	TGCTTCTGCTTTCGTAGCGCGCATCGCTGGAGCGGCTGTGGCAGATAGGCTTGG	7346
QY	4260	GAAGGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCTGTGC	4319
Db	7347	GAAGGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCTGTGC	7406
QY	4320	CTTTAAGGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGCTAACTACTCTCTGC	4379

Db	7407	CTTTAAGGTCATGAGCGCGGAGATGCCCTCCACGAGGACCTGGTTAACTACTTCCCTGCG	7466	8487	CCTCATCAGGCCCAACCTCTGTGTGGCGCAGGAGATGGGCGGGAAACATCATCCCGCGTGGG	8546
Qy	4380	TATCCTCTCCCTCGCGCGCCCTGAGTCTGCGGGTCTGTCGCGACGATGATCTGCGTCCGCA	4439	5460	GTGAGAAAATAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCCAAGCGAGGAGGATGA	5519
Db	7467	TATCCTCTCCCTCGCGCGCCCTGAGTCTGTCGCGGGTCTGTCGCGACGATGATCTGCGTCCGCA	7526	8547	GTGAGAAAATAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCCAAGCGAGGAGGATGA	8606
Qy	4440	CGTGGGCGCAGGGGAGGGGCTGTGCAATGATGAAACCGGTGTATGAGGTTTCGCTTCGCG	4499	5520	GAGGAAAGTATCCGTTTCGCGCGGAGATCTCTCGGAGGTCCAGGAAATTCCTCTCAGGCGAT	5579
Db	7527	CGTGGCGCCAGGGGAGGGGCTGTGCAATGATGAAACCGGTGTATGAGGTTTCGCTTCGCG	7586	8607	GAGGAAAGTATCCGTTTCGCGCGGAGATCTCTCGGAGGTCCAGGAAATTCCTCTCAGGCGAT	8666
Qy	4500	GGGTAAACAGTCTCCCGCAGCACTATGTCCTGAGAGCAGCGCTGAGCAGCTGTCTAC	4559	5580	GCCCATATGGGCAACGCCGGATTAACAACCTCTCAGTCTAGAGTCTCTGAGAGGACCCGGA	5639
Db	7587	GGGTAAACAGTCTCCCGCAGCACTATGTCCTGAGAGCAGCGCTGAGCAGCTGTCTAC	7646	8667	GCCCATATGGGCAACGCCGGATTAACAACCTCTCAGTCTAGAGTCTCTGAGAGGACCCGGA	8726
Qy	4560	TCAGATCTCTCTAGTCTTACATCACTCAGTCTGCTGAAGAGGCTTCCACAGTGGATCAA	4619	5640	CTAGTCTCTCTCAGTCTTACACGCGGTGTCATTCGCGCTCCCAAGGCCCTCTCGATACC	5699
Db	7647	TCAGATCTCTCTAGTCTTACATCACTCAGTCTGCTGAAGAGGCTTCCACAGTGGATCAA	7706	8727	CTAGTCTCTCTCAGTCTTACACGCGGTGTCATTCGCGCTCCCAAGGCCCTCTCGATACC	8786
Qy	4620	CGAGGACTGCTCCACGCGCATGCTCCGGTCTGTCGCTAAGAGATGTTTGGGATGGATATG	4679	5700	ACCTCCAGGAGGAGGACGGTGTCTCTGTCAAGATCTTACCGTGTCTTCTGCTTGGC	5759
Db	7707	CGAGGACTGCTCCACGCGCATGCTCCGGTCTGTCGCTAAGAGATGTTTGGGATGGATATG	7766	8787	ACCTCCAGGAGGAGGACGGTGTCTCTGTCAAGATCTTACCGTGTCTTCTGCTTGGC	8846
Qy	4680	CACGCTGTGACTGATTTTCAAGACCTGCTCCAGTCCAGTCTCTGCGCGGATTCGCGGG	4739	5760	GGAGCTCCCAACAAAGACCTTTCGAGCTCCGAATCGTGGCGCTCGACAGCGCACCGC	5819
Db	7767	CACGCTGTGACTGATTTTCAAGACCTGCTCCAGTCCAGTCTCTGCGCGGATTCGCGGG	7826	8847	GGAGCTCCCAACAAAGACCTTTCGAGCTCCGAATCGTGGCGCTCGACAGCGCACCGC	8906
Qy	4740	AGTCCCTCTCTCTCATGTCACAGCTGGGTACAAGGAGTCTGCGCGGGCGAGCGGATCAT	4799	5880	CTCTCTCATGTCCTTGAAGGGAGCGCGGGGATCCCGATCTCAGGAGCGGTCTTG	5939
Db	7827	AGTCCCTCTCTCTCATGTCACAGCTGGGTACAAGGAGTCTGCGCGGGCGAGCGGATCAT	7886	8967	CTCTCTCATGTCCTTGAAGGGAGCGCGGGGATCCCGATCTCAGGAGCGGTCTTG	9026
Qy	4800	GCAAAACCACTGCTCCATGTCGAGTCAACCGGACATGTGAAAAGGTTTCCATGAG	4859	5940	GTCTACCGTAAAGGAGGCTAGTGAAGAGCTCTCTGCTGCTCGATGCTCTACACATG	5999
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Qy	4860	GATCGTGGGCTTAGGACTGATGTAACGCGATGGAACATTTCCCATTAACCGCTA	4919	6000	GACAGCGCCCTGATCAGCCATGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACT	6059
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Qy	4920	CACACGGGCGCTGTCAGCGCTCCCGCGCGCAAAATTTATTCAGGCGCTGTGCGGGT	4979	6060	GAGCAATCTTTGCTCCGTCACCAAACTTTGCTATGTATGTAACAACTCTCGAGCGCAAG	6119
Db	8007	CACACGGGCGCTGTCAGCGCTCCCGCGCGCAAAATTTATTCAGGCGCTGTGCGGGT	8066	9147	GAGCAATCTTTGCTCCGTCACCAAACTTTGCTATGTATGTAACAACTCTCGAGCGCAAG	9206
Qy	4980	GGCTGCTGAGGAGTACGTGAGGTTACGGGGTGGGGATTTCCACTACGTACGGGCAT	5039	6120	CCTGCGGAGAAAGAGTCACTTTGACAGATCTGAGGCTCTGGAACCACTTACCGGGA	6179
Db	8067	GGCTGCTGAGGAGTACGTGAGGTTACGGGGTGGGGATTTCCACTACGTACGGGCAT	8126	9207	CCTGCGGAGAAAGAGTCACTTTGACAGATCTGAGGCTCTGGAACCACTTACCGGGA	9266
Qy	5040	GACCACTGACAAAGTAAAGTCCCGTTCAGGTTCCCGGCCCGCAATTTCTCACAGAAT	5099	6180	CGTGTCTCAAGGAGATGAAGCGGAGGCTCCACAGTTAAGGCTAAATTTCTATCCGTGA	6239
Db	8127	GACCACTGACAAAGTAAAGTCCCGTTCAGGTTCCCGGCCCGCAATTTCTCACAGAAT	8186	9267	CGTGTCTCAAGGAGATGAAGCGGAGGCTCCACAGTTAAGGCTAAATTTCTATCCGTGA	9326
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Qy	5160	CACATTCCTGCTGGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATGCGAGCCCGA	5219	6300	GGAGCTCCGGAACCTATCAGCAAGCGCTTAAACCACTCCGCTCCGCTGTGGAAGGACTT	6359
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RESULT 9

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US-09-539-601-25
; Sequence 25, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 11076
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/Core-3'/5.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(10845)
; OTHER INFORMATION: hepatitis C virus polyprotein from core to
; OTHER INFORMATION: nonstructural protein NS5B, carries cell
; OTHER INFORMATION: culture-adaptive mutations of clone 5.1
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (10846)..(11076)
US-09-539-601-25
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Query Match

77.1%; Score 6162.8; DB 4; Length 11076;

Best Local Similarity 99.7%; Pred. No. 0; Matches 6173; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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QY 1860 TAGCCTCACAGCGCGGAGACAGAACCAAGTTCGAGGGGAGTCCAGTGGTCTCCACGCG 1919
DB 4947 TAGCCTCACAGCGCGGAGACAGAACCAAGTTCGAGGGGAGTCCAGTGGTCTCCACGCG 5006
QY 1920 AACCAATCTTCTGGGACCTCGTCAATGGGCTGTGGTGGACTGTCTATCATGTGTC 1979
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QY 1980 CGGCTCAAGACCTTTCGCGGCCCAAGGGGCCCAATCAACCAATGTATACCAATGTGGA 2039
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Db	7107	GTGGAATTTTCATCAGCGGGATACAAATATTTAGCAGGCTTTGCCACTCTGCTGCGCAACCC	7166
QY	4080	CGCGATAGCATCACTGATGGCAATTCACAGCTCTATACAGCGCCGCTCACCAACCAACA	4139
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QY	4140	TACCTCTCTGTTTAACTCTGGGGGATGGGTGGCGCCCACTTCTCTCTCCAGCGC	4199
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Db	7707	CGAGGACTGCTCCACGGCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGATTTGGATATG	7766
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Db	7887	GCAAACCACTGCGCATGTGGGAGCACAGATCACCGGACATGTGMAAAAGTTTCCATGAG	7946
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QY	5160	CACATTTCTGCTCGGGCTCAATCAATACCTGCTTGGGTTCACAGCTCCCATGCGAGCCCGA	5219
Db	8247	CACATTTCTGCTCGGGCTCAATCAATACCTGCTTGGGTTCACAGCTCCCATGCGAGCCCGA	8306
QY	5220	ACCGGAGTACAGTGTCTCACTTCCATGCTCACGACCCCTCCCAATTAAGCGGAGAC	5279
Db	8307	ACCGGAGTACAGTGTCTCACTTCCATGCTCACGACCCCTCCCAATTAAGCGGAGAC	8366
QY	5280	GGCTAAGCGTAGGCTGSCCAGGGGATCTCCCTCTCTGGCCAGCTCATCAGCTAGCCA	5339
Db	8367	GGCTAAGCGTAGGCTGSCCAGGGGATCTCTCTCTCTGGCCAGCTCATCAGCTAGCCA	8426
QY	5340	GCTGTCTGCGCCCTTCTTGAAGGCAACATGCACTACCGGTCATGACTCCCGGACGCTGA	5399
Db	8427	GCTGTCTGCGCCCTTCTTGAAGGCAACATGCACTACCGGTCATGACTCCCGGACGCTGA	8486
QY	5400	CCTCATCGAGGCCAACCTCTCTGTGGCGGACAGATGGGCGGAAACATCACCCCGCTGGA	5459
Db	8487	CCTCATCGAGGCCAACCTCTCTGTGGCGGACAGATGGGCGGAAACATCACCCCGCTGGA	8546
QY	5460	GTGAGAAATAAGTAGTAGTAAATTTTGGACTCTTTCGAGCGGCTCCAAAGCGGAGGATGA	5519
Db	8547	GTGAGAAATAAGTAGTAGTAAATTTTGGACTCTTTCGAGCGGCTCCAAAGCGGAGGATGA	8606
QY	5520	GAGGGAAGTATCCGTTCCGCGGAGATCTCTGCGGAGTCCAGGAAATTCCTCTCGAGCAT	5579
Db	8607	GAGGGAAGTATCCGTTCCGCGGAGATCTCTGCGGAGTCCAGGAAATTCCTCTCGAGCAT	8666
QY	5580	GCCCATATGGGACGCGCCGGATTAACAACTCTCACTGTTAGAGTCTCTGGAAGAACCCGGA	5639
Db	8667	GCCCATATGGGACGCGCCGGATTAACAACTCTCACTGTTAGAGTCTCTGGAAGAACCCGGA	8726
QY	5640	CTACGTCCTCTCAGTGTGATACAGGGTGTCCATTTGCGGCTGCCAAGCGCCCTCCGATACC	5699
Db	8727	CTACGTCCTCTCAGTGTGATACAGGGTGTCCATTTGCGGCTGCCAAGCGCCCTCCGATACC	8786
QY	5700	ACTTCCACGAGGAGGACGAGGACGCTTCTCTGTGAGAAATCTACCGTGTCTTCTGCTTGGC	5759
Db	8787	ACTTCCACGAGGAGGACGAGGACGCTTCTCTGTGAGAAATCTACCGTGTCTTCTGCTTGGC	8846
QY	5760	GGAGCTCGGACAAAGACCTTGGGAGCTCCGAAATGCTGCGCGCTCGACAGCGGACCGGC	5819
Db	8847	GGAGCTCGGACAAAGACCTTGGGAGCTCCGAAATGCTGCGCGCTCGACAGCGGACCGGC	8906
QY	5820	AACGGGCTCTCTGACAGCCCTTCGACGACGCGGAGTCCGAGCTTGGAGTCTGTA	5879
Db	8907	AACGGGCTCTCTGACAGCCCTTCGACGACGCGGAGTCCGAGCTTGGAGTCTGTA	8966
QY	5880	CTCTCTCATGCCCCCTTTGAGGGGAGCGGGGGATCCCGATCTCAGCGAGCGGCTCTTG	5939
Db	8967	CTCTCTCATGCCCCCTTTGAGGGGAGCGGGGGATCCCGATCTCAGCGAGCGGCTCTTG	9026
QY	5940	GTCTACCGTAAGCGAGGAGGCTAGTGAGGACGTGCTGCTGCTGCTGATGCTTACATG	5999
Db	9027	GTCTACCGTAAGCGAGGAGGCTAGTGAGGACGTGCTGCTGCTGCTGATGCTTACATG	9086
QY	6000	GACGCGCCCTGATACGCCATGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACT	6059
Db	9087	GACGCGCCCTGATACGCCATGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACT	9146
QY	6060	GAGCAACTCTTTGCTCCGTACCAAACTTGGTCTATGCTCAAAATCTCGCAGGCGCAAG	6119
Db	9147	GAGCAACTCTTTGCTCCGTACCAAACTTGGTCTATGCTCAAAATCTCGCAGGCGCAAG	9206
QY	6120	CCTGGGAGGAGGATCACTTTGACAGACTGCGAGGTCCTGGAGCACCACTACCGGGA	6179

Db	9207	 CCTCGGCAGAAAGGTCACCTTTGACAGACTGCGGTCTCTGGACGACCACTACCGGGA	9266
Qy	6180	CGTGTCTAAGGAGATGAAGGCGAAGGCGTCACAGTTAAGCTAAACTCTATCCGTGGA	6239
Db	9267	CGTGTCTAAGGAGATGAAGGCGAAGGCGTCACAGTTAAGCTAAACTCTATCCGTGGA	9326
Qy	6240	GGAGCGCTCTAAGCTTCAGCCGCCACATTCGGGCGAGATCTAAATTTGGCTATGGGGCAAA	6299
Db	9327	GGAGCGCTCTAAGCTTCAGCCGCCACATTCGGGCGAGATCTAAATTTGGCTATGGGGCAAA	9386
Qy	6300	GGAGCTCCGGAAACCTATTCAGCAAGGCGGTTAAACCACATCCGCTCCGTGTGGAAGGACTT	6359
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Db	9447	GCTGGAAGACACTGAGACACCAATTTGACACACACATCATGGCAAAAATGAGGTTTTCTG	9506
Qy	6420	CGTCCAAACAGAGAAGGGGGCGCAAGCGAGCTCGCTTATCGTATTCCAGATTTGGG	6479
Db	9507	CGTCCAAACAGAGAAGGGGGCGCAAGCGAGCTCGCTTATCGTATTCCAGATTTGGG	9566
Qy	6480	GGTTCGTGTGTCGGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCCGT	6539
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Qy	6540	GATGGGCTCTTCATACGGATTCGAATATCTCTCTCGGACAGGGGTCGAGTTCTTGTTGAA	6599
Db	9627	GATGGGCTCTTCATACGGATTCGAATATCTCTCTCGGACAGGGGTCGAGTTCTTGTTGAA	9686
Qy	6600	TGCTCGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTGACTC	6659
Db	9687	TGCTCGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTGACTC	9746
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Qy	6780	GACTAATCTTAAAGGCGAAGCTCGCGCTATCGCGGTCCGCGCGAGCGGTGACTGAC	6839
Db	9867	GACTAATCTTAAAGGCGAAGCTCGCGCTATCGCGGTCCGCGCGAGCGGTGACTGAC	9926
Qy	6840	GACCAGTCGGGTAAATACCCCTCACATGTTACTTGAAGCCGCTCGGGCTGTFCGAGTGC	6899
Db	9927	GACCAGTCGGGTAAATACCCCTCACATGTTACTTGAAGCCGCTCGGGCTGTFCGAGTGC	9986
Qy	6900	GAAGCTCCAGACTGACAGATGCTGTATCGGAGACGACCTTGTGCTTATCTGTGAAAG	6959
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Db	10047	CGCGGAGACCAAGAGAGACGAGCGAGCCTACGGGCTTCA CGGAGGCTATGACTAGATA	10106
Qy	7020	CTCTGCCCCCTCGGGACCCGCCAAACAGAAATACGACTTGGAGTTGATAAATCATG	7079
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Qy	7080	CTCCTCAATGTGTCACTCGCGACGATGCATCTGGCAAAAGGTGTACTATCTCACCCG	7139
Db	10167	CTCCTCAATGTGTCACTCGCGACGATGCATCTGGCAAAAGGTGTACTATCTCACCCG	10226
Qy	7140	TGACCCACACACCCCTTCGCGGGGCTGGTGGGAGACAGCTAGACACACTCCAGTCAA	7199
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Db	10287	TTCTCGGCTGAGCAACATCATCATGTATGCGCCACCCTTGTGGCAAGGATGATCCTTGAT	10344
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Db	10347	GACTCATTTCTTCTCCATCCTTTAGCTCAGGAACAACCTTGAAAAGCCCTAGATTGTCA	10406
Qy	7320	GACTACGGGGCGCTGTACTCATTGAGCGCACTTGACCTACTCAGATCATTTCAACGACT	7379
Db	10407	GATCTACGGGGCGCTGTATTCTCCATTGAGCCACTTGACCTACTCAGATCATTTCAACGACT	10466
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Db	10467	CCATGGCCCTTAGCGCAATTTTCACTCCATAGTTACTTCTCCAGGTGAGATCAATAGGGTGGC	10526
Qy	7440	TTCATGCCCTCAGGAACCTTGGGGTACCGCCCTTGGAGCTCTGGAGACATCGGGCGCAGAAG	7499
Db	10527	TTCATGCCCTCAGGAACCTTGGGGTACCGCCCTTGGAGCTCTGGAGACATCGGGCGCAGAAG	10586
Qy	7500	TGTCGCGGCTAGGCTACTGTCTCCAGGGGGGAGGGCTCGCACTTGTGCAAGTACTTCTT	7559
Db	10587	TGTCGCGGCTAGGCTACTGTCTCCAGGGGGGAGGGCTCGCACTTGTGCAAGTACTTCTT	10646
Qy	7560	CAACTGGCAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGTGGGTCCCAAGTTGGA	7619
Db	10647	CAACTGGCAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGTGGGTCCCAAGTTGGA	10706
Qy	7620	TTTTATCCAGCTGGTTCGTTGCTGTGTACAGCGGGGAGACATATATCAACGCTGTCTCG	7679
Db	10707	TTTTATCCAGCTGGTTCGTTGCTGTGTACAGCGGGGAGACATATATCAACGCTGTCTCG	10766
Qy	7680	TGCCGACCCGCTGGTTCATCTGGTGCTACTCTCTACTTTCGTAGGGGTAGGCATCTA	7739
Db	10767	TGCCGACCCGCTGGTTCATCTGGTGCTACTCTCTACTTTCGTAGGGGTAGGCATCTA	10826
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Db	10827	TCTACTCCCCAAACCGATGAACGGGAGCTAATAACACTCCAGGCCAATAGGCCATCTGTTT	10886
Qy	7800	TTTTCCGCTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCCTTT	7859
Db	10887	TTTTCCGCTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCCTTT	10946
Qy	7860	TTTTTTTCTTTTTTTTTTCTTTTTTCTTTTCTTTGGTGCTCCATCTTAGCCCTAGTCACGG	7919
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Qy	7920	CTAGCTGTGAAAGGTCGGTAGCCGCTTGACTCGAGAGTGTCTGATCTAGCCCTCTCTG	7979
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Db	11067	CAGATCAAGT	11076

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RESULT 10
US-09-539-601-19
; Sequence 19, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschlagger, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11076
; TYPE: DNA
; ORGANISM: Hepatitis C virus

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; FEATURE:
; NAME/KEY: 5' UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct 1389/Core-3//9-13F
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
;
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(10845)
; OTHER INFORMATION: hepatitis C virus polyprotein from core to
; OTHER INFORMATION: nonstructural protein NS5B; carries cell
; OTHER INFORMATION: culture-adaptive mutations from clone 9-13F
;
; FEATURE:
; NAME/KEY: 3' UTR
; LOCATION: (10846)..(11076)
;
US-09-539-601-19

Query Match
Best Local Similarity 77.1%; Score 6161.2; DB 4; Length 11076;
Matches 6172; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1800 CATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCAC 1859
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QY 1860 TAGCCTCACAGGCGCGACAGGACCAAGTTCGAGGGGAGGTCCAGTGTCTCCACCGC 1919
DB 4947 TAGCCTCACAGGCGCGACAGGACCAAGTTCGAGGGGAGGTCCAGTGTCTCCACCGC 5006

QY 1920 AACACAATCTTCTGGCGACCTGCGTCAATGGCGTGTGTGGACTCTCTATCATGTGC 1979
DB 5007 AACACAATCTTCTGGCGACCTGCGTCAATGGCGTGTGTGGACTCTCTATCATGTGC 5066

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DB 5187 CGGAGCTCGGACCTTTACTTGGTTCAGAGGCAATGCCGATGTCATTCGGGTGGCGCGG 5246

QY 2160 GGGCGACAGCGGGGAGGCTACTCTCCCGCGGCGGCTCTCTACTTGAAGGGCTCTTC 2219
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DB 5427 GGGGTCCCGGCTCTTTCAGCGAATCTGTCCTCCCTCCGCGGCTACCGACACATTCAGGT 5486

QY 2400 GGGCCATCTACAGCGCCCTACTGTAGCGGACAGACACTAAGGTCCCGGCTGCATGTC 2459
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Db	6687	GTATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACACACACCCCAATAACAT	7767	CACGGTGTGACTGATTTTCAAGACTCGCTCCAGTCCAAAGCTCTCCGCGGATTCGCGGG	7826
Qy	3660	CATGGCATGATGTGGCTGACCTGGAGGTCGTCAACGAGCACCCTGGGTGCTGGTAGGCGG	4740	AGTCCCCCTTCTTCATGTCAAACGTGGGTCAAAGGAGTCTGGCGGGGCGACGGCATCAT	4799
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Qy	3720	AGTCTAGCAGCTCTGGCGCGGATTTGCTGACACAGGAGCGGTGTCATTTGGGCGAG	4800	GCAAAACCACTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAAAGTTTCCATGAG	4859
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Qy	3780	GATCATCTTGTCCGGAAGCGCGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTT	4860	GATCGTGGGCTTAGGACCTCTAGTAAACAGCTGGCATGGAACATTTCCCAATTAAACCGCTA	4919
Db	6867	GATCATCTTGTCCGGAAGCGCGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTT	7947	GATCGTGGGCTTAGGACCTCTAGTAAACAGCTGGCATGGAACATTTCCCAATTAAACCGCTA	8006
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Db	6927	CGATGAGATGGAAGTGGGCTCAACCTCCCTTACATCGAACAGGGAATGACAGTCCG	8007	CACCAACGCGCCCTGACGCGCTCCCGCGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGT	8066
Qy	3900	CGAAACAATCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGC	4980	GGCTGCTGAGGAGTACGTGGAGTTTACCGGGTGGGGATTTTCCACTAGCTGACCGGGCAT	5039
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Qy	4080	CGCGATAGCATCACTGATGGGATTTAGAGGTTGTCCACTCTGCTCTGGCAACCC	5160	CACATTTCTGCTGGCTCAATCAATACCTGCTGGGTCACAGTCCCATTCGAGAGCCGA	5219
Db	7167	CGCGATAGCATCACTGATGGGATTTAGAGGTTGTCCACTCTGCTCTGGCAACCC	8247	CACATTTCTGCTGGCTCAATCAATACCTGCTGGGTCACAGTCCCATTCGAGAGCCGA	8306
Qy	4140	TACCTCTCTGTTTAAACATCTCGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGC	5220	ACCGAGCTGAGGCTGCTACCTTCCATGCTCACAGCAGCCCTCCCACTTACCGCGGAGAC	5279
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Qy	4200	TGCTTCTGTTTCTGATAGGCGCGGATTCGCTGAGCGGCTGTGGAGCATAGGCTTGG	5280	GGCTAAGCTGAGGCTGGCGAGGGGATCTCCCGCTCTTGGCCAGCTCATAGCTAGGCCA	5339
Db	7287	TGCTTCTGTTTCTGATAGGCGCGGATTCGCTGAGCGGCTGTGGAGCATAGGCTTGG	8367	GGCTAAGCTGAGGCTGGCGAGGGGATCTCCCGCTCTTGGCCAGCTCATAGCTAGGCCA	8426
Qy	4260	GAGGCTGCTGTGGATTTTGGCAGGTTTATGGAGCAGGCTGGCAGCGCGCTCGTGGC	5340	GCTGCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGACCTGA	5399
Db	7347	GAGGCTGCTGTGGATTTTGGCAGGTTTATGGAGCAGGCTGGCAGCGCGCTCGTGGC	8427	GCTGCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGACCTGA	8486
Qy	4320	CTTTAAGGTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGCTAACTCTCCCTGC	5400	CCTCATCGAGGCAACCTCTGCGCGCAGGAGATGGGCGGGGAAACATCACCGCGGTGA	5459
Db	7407	CTTTAAGGTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGCTAACTCTCCCTGC	8487	CCTCATCGAGGCAACCTCTGCGCGCAGGAGATGGGCGGGGAAACATCACCGCGGTGA	8546
Qy	4380	TATCTCTCCCTGGCGCCCTAGTCTGCGGGTCTGTGGCAGCGCATATGCTGGCGCA	5460	GTCAAGAAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCGCTCCAAAGCGGAGGATGA	5519
Db	7467	TATCTCTCCCTGGCGCCCTAGTCTGCGGGTCTGTGGCAGCGCATATGCTGGCGCA	8547	GTCAAGAAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCGCTCCAAAGCGGAGGATGA	8606
Qy	4440	CGTGGGCGCAGGGGCGGCTGTGAGTGGATGAAACCGGCTCATAGCGTTCCCTTCGCG	5520	GAGGGAAGTATCCGTTCCGCGGAGATCTGCGGAGTCCAGGAAATTCCTTCGAGCGAT	5579
Db	7527	CGTGGGCGCAGGGGCGGCTGTGAGTGGATGAAACCGGCTCATAGCGTTCCCTTCGCG	8607	GAGGGAAGTATCCGTTCCGCGGAGATCTGCGGAGGTCAGGAAATTCCTTCGAGCGAT	8666
Qy	4500	GGGTAAACCAAGCTCTCCCGACGACATATGTGCTGAGAGCGACGCTGACGACGTTGAC	5580	GCCCATATGGGCAACCGCGGATTTACAAACCTCCACTGTTTAGAGTCTCTGGAAGACCCGA	5639
Db	7587	GGGTAAACCAAGCTCTCCCGACGACATATGTGCTGAGAGCGACGCTGACGACGTTGAC	8667	GCCCATATGGGCAACCGCGGATTTACAAACCTCCACTGTTTAGAGTCTCTGGAAGACCCGA	8726
Qy	4560	TCAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCCACAGTGGATCAA	5640	CTACGTCCTTCCAGTGGTACAACGGGTGTCATTTGCGCGCTGCAAGGCCCTTCGATACC	5699
Db	7647	TCAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCCACAGTGGATCAA	8727	CTACGTCCTTCCAGTGGTACAACGGGTGTCATTTGCGCGCTGCAAGGCCCTTCGATACC	8786
Qy	4620	CGAGGACTGCTCCACGCGCATGCTCCGCGCTCGTGGCTAAGAGATGTTTGGGATGGATATG	5700	ACCTCCACCGGGAAGGAGCGGTTCTGCTGAGAAATCTACCGTGTCTTCTGCTTGGC	5759
			8787	ACCTCCACCGGGAAGGAGCGGTTGCTGCTGAGAAATCTACCGTGTCTTCTGCTTGGC	8846

Db	11007	CTAGCTGTGAAGTTCGGTGGAGCGCTGACTGCAGAGAGTGTCTGATACTGGCCTCTCTG	11066
Qy	7980	CAGATCAAGT 7989	
Db	11067	CAGATCAAGT 11076	
RESULT 11			
US-09-539-601-31			
; Sequence 31, Application US/09539601C			
; Patent No. 6630343			
; GENERAL INFORMATION:			
; APPLICANT: Bartenschlager, Ralf FW			
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System			
; FILE REFERENCE: all sequences			
; CURRENT APPLICATION NUMBER: US/09/539,601C			
; CURRENT FILING DATE: 2001-08-30			
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY			
; EARLIER FILING DATE: 1999-04-03			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 31			
; LENGTH: 11076			
; TYPE: DNA			
; ORGANISM: Hepatitis C virus			
; FEATURE:			
; NAME/KEY: 5'UTR			
; LOCATION: (1)..(341)			
; OTHER INFORMATION: construct I389/Core-3'/19			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (342)..(1193)			
; OTHER INFORMATION: hepatitis C virus core - neomycin			
; OTHER INFORMATION: phosphotransferase fusion protein			
; FEATURE:			
; NAME/KEY: RBS			
; LOCATION: (1202)..(1812)			
; OTHER INFORMATION: internal ribosome entry site from			
; OTHER INFORMATION: encephalomyocarditis virus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1813)..(10845)			
; OTHER INFORMATION: hepatitis C virus polypeptide from core to			
; OTHER INFORMATION: nonstructural protein NS5B; carries cell culture			
; OTHER INFORMATION: adaptive mutations from clone no. 19			
; FEATURE:			
; NAME/KEY: 3'UTR			
; LOCATION: (10846)..(11076)			
US-09-539-601-31			
Query Match			
Best Local Similarity 99.6%; Pred. No. 0;			
Matches 6168; Conservative 0; Mismatches 22; Indels 0; Gaps 0;			
Qy	1800	CATGGCGCCTATTACGGCCTACTCCACAGACGCGAGGCTACTTGGCTGCATCATCAC	1959
Db	4887	CCTCGCGCCTATTACGGCCTACTCCACAGACGCGAGGCTACTTGGCTGCATCATCAC	4946
Qy	1860	TAGCCTCACAGGCGGAGACAGGACAGGTCGAGGGGAGGTCCAGGTGCTCTCCACCGC	1919
Db	4947	TAGCCTCACAGGCGGAGACAGGACAGGTCGAGGGGAGGTCCAAAGTGTCTCCACCGC	5006
Qy	1920	AACACAATTTCTTCTGGCGACTGCGTCAATGGCGTGTGGACTGTCTATCATGTGC	1979
Db	5007	AACACAATTTCTTCTGGCGACTGCGTCAATGGCGTGTGGACTGTCTATCATGTGC	5066
Qy	1980	CGSCTCAAGACCTTCGCGCCCAAGGCGCAATCAACCAATGTACACCAATGTGA	2039
Db	5067	CGSCTCAAGACCTTCGCGCCCAAGGCGCAATCAACCAATGTACACCAATGTGA	5126
Qy	2040	CCAGGACTCTGTCGGCTGGCAAGCGCCCGCGCGCTTCTTGTGACACCATGACCTG	2099

5127	CCAGGACCTCGTGGCTGGCAAGCGCCCGCGCGCGCTTCTTGTGACACATGCACTG	5186
2100	CGGAGCTTCGGACCTTTTACTTGTTCAGAGCATGCGATGTCATTCGGTGCCTCGCGG	2159
5187	CGGAGCTTCGGACCTTTTACTTGTTCAGAGCATGCGATGTCATTCGGTGCCTCGCGG	5246
2160	GGGCGACAGCAGGGGAGCGCTTCTCCCCAGGCCCGTCTCTTCTTGAAGGCTCTTC	2219
5247	GGGCGACAGCAGGGGAGCGCTTCTCCCCAGGCCCGTCTCTTCTTGAAGGCTCTTC	5306
2220	GGGCGTCCACTGCTGCTGCGGCGACGCTGTGGGCACTTTTGGGCTCGCGTGTG	2279
5307	GGGCGTCCACTGCTGCTGCGGCGACGCTGTGGGCACTTTTGGGCTCGCGTGTG	5366
2280	CACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCGCTCGAGTCTATGGAACCACTAT	2339
5367	CACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCGCTCGAGTCTATGGAACCACTAT	5426
2340	CGGCTCCCGGCTTTCACGACAACTCGTCCCTCGGCCGTACCGGAGACATTCAGGT	2399
5427	CGGCTCCCGGCTTTCACGACAACTCGTCCCTCGGCCGTACCGGAGACATTCAGGT	5486
2400	GGCCCATCTACAGCCCTTCTGCTAGCGGCAAGGACGCTAAGGTGCGGCTGCTATGC	2459
5487	GGCCCATCTACAGCCCTTCTGCTAGCGGCAAGGACGCTAAGGTGCGGCTGCTATGC	5546
2460	AGCCCAAGGTTAAGGTGCTTCTCTGAACCGCTCGCGCGCACCCCTAGGTTTCGG	2519
5547	AGCCCAAGGTTAAGGTGCTTCTCTGAACCGCTCGCGCGCACCCCTAGGTTTCGG	5606
2520	GGCGTATATGCTAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTGAAGACCAT	2579
5607	GGCGTATATGCTAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTGAAGACCAT	5666
2580	CACCGAGGTTGCCCCCATCAGTACTCCACCTATGCGAAGTTCTTCCGCGAGGTGTTG	2639
5667	CACCGAGGTTGCCCCCATCAGTACTCCACCTATGCGAAGTTCTTCCGCGAGGTGTTG	5726
2640	CTCTGGGCGGCTATGATCATATAATGATGATGCTGCTGCTCAACTCACTGACACAC	2699
5727	CTCTGGGCGGCTATGATCATATAATGATGATGCTGCTGCTCAACTCACTGACACAC	5786
2700	TATCTGGGCTCGGCACAGTCTCTGGAACAGCGGAGCGGTGAGCGCGACTCGTCTG	2759
5787	TATCTGGGCTCGGCACAGTCTCTGGAACAGCGGAGCGGTGAGCGCGACTCGTCTG	5846
2760	GCTCGCCACCGCTACGCTTCCGGATCCGTCACCGTGCACATCCAAACATCAGGAGGT	2819
5847	GCTCGCCACCGCTACGCTTCCGGATCCGTCACCGTGCACATCCAAACATCAGGAGGT	5906
2820	GGCTGTCTCAGCAGTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCAT	2879
5907	GGCTGTCTCAGCAGTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCAT	5966
2880	CAGGGGGGAGGACCTCATTTTCTGCCATTCCTCAAGAGAAATGATGATGCTCGCGC	2939
5967	CAGGGGGGAGGACCTCATTTTCTGCCATTCCTCAAGAGAAATGATGATGCTCGCGC	6026
2940	GAAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCCGT	2999
6027	GAAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCCGT	6086
3000	CATACCAATAGCGGAGAGCTCAATGCTGTAGCAACCGGAGCTCTTAATGCGGGCTTTAC	3059
6087	CATACCAATAGCGGAGAGCTCAATGCTGTAGCAACCGGAGCTCTTAATGCGGGCTTTAC	6146
3060	CGGGAATTCGACTGAGTGCATGCTGCATATGCTGTCACCGAGAGCTGCACTTCAG	3119
6147	CGGGAATTCGACTGAGTGCATGCTGCATATGCTGTCACCGAGAGCTGCACTTCAG	6206
3120	CCTGGACCCGACTTTCACCATTCAGACGAGCGCTGCCCAAGAGCGGCTGTCAGGCTC	3179
6207	CCTGGACCCGACTTTCACCATTCAGACGAGCGCTGCCCAAGAGCGGCTGTCAGGCTC	6266

QY	3180	GCAGCGCGAGCAGCACTGGTAGCGGCAGGATGGCCATTTTACAGETTTGTGATCTCCAGG	3239
Db	6267	GCAGCGCGAGCAGCAGCACTGGTAGGGGACGGATGGGCAITTTACAGTTTGTGATCTCAGG	6326
QY	3240	AGAAACGGCCCTCGGCATGTTTCGATTCTCTCGGTTCTGTGCGAGTGTCTATGACGCGGCGTG	3299
Db	6327	AGAAACGGCCCTCGGCATGTTTCGATTCTCTCGGTTCTGTGCGAGTGTCTATGACGCGGCGTG	6386
QY	3300	TGCTTTGGTAGAGCTACGCGCGCGGAGACCTCAGTAGTGTTCGGGGCTTACCTAAACAC	3359
Db	6387	TGCTTTGGTAGAGCTACGCGCGCGGAGACCTCAGTAGTGTTCGGGGCTTACCTAAACAC	6446
QY	3360	ACCAGGGTTGCCGCTCTGCCAGGACCACTGCGAGTTCTGGGAGAGCGTCTTTTACAGGCT	3419
Db	6447	ACCAGGGTTGCCGCTCTGCCAGGACCACTGCGAGTTCTGGGAGAGCGTCTTTTACAGGCT	6506
QY	3420	CACCCACATAGACGCCCATTTCTTGTCCTCCAGACTAAGCAGGACGACAACTTCCCTTA	3479
Db	6507	CACCCACATAGACGCCCATTTCTTGTCCTCCAGACTAAGCAGGACGACAACTTCCCTTA	6566
QY	3480	CTGTGTAGCATACCAAGGCTACGCTGTGGCCAGGGCTCAGGCTCCACTCCATGTGTGGGA	3539
Db	6567	CTGTGTAGCATACCAAGGCTACGCTGTGGCCAGGGCTCAGGCTCCACTCCATGTGTGGGA	6626
QY	3540	CCAAATGTGGAAGTGTCTCATACGGCTAAAGCCTTACGCTGCAGGGGCCAAGCCCTGCT	3599
Db	6627	CCAAATGTGGAAGTGTCTCATACGGCTAAGCCTTACGCTGCAGGGGCCAAGCCCTGCT	6686
QY	3600	GTATAGGCTGGAGCGGTTCCAAACGAGGTTTACTACCAACCCCATACCAAAATACAT	3659
Db	6687	GTATAGGCTGGAGCGGTTCCAAACGAGGTTTACTACCAACCCCATACCAAAATACAT	6746
QY	3660	CATGGCATGCATGCGCTGACCTCGAGGTGCTGACGAGCACTGGGTGCTGTGAGCGG	3719
Db	6747	CATGGCATGCATGCGCTGACCTCGAGGTGCTGACGAGCACTGGGTGCTGTGAGCGG	6806
QY	3720	AGTCTTAGCAGCTCTGGCCGCGTATTGCCCTGACAAACAGGACGCTGTCTATTGTGGGAG	3779
Db	6807	AGTCTTAGCAGCTCTGGCCGCGTATTGCCCTGACAAACAGGACGCTGTCTATTGTGGGAG	6866
QY	3780	GATCATCTTGTCCGGAAGCGCGGCATCATTCOCGACAGGAAGTCTTTTACCGGAGTT	3839
Db	6867	GATCATCTTGTCCGGAAGCGCGGCATCATTCOCGACAGGAAGTCTTTTACCGGAGTT	6926
QY	3840	CGATGAGATGGAAGGTGCGCCTCACACCTCCCTTACATCGACAGGGAATGCAGCTCGC	3899
Db	6927	CGATGAGATGGAAGGTGCGCCTCACACCTCCCTTACATCGACAGGGAATGCAGCTCGC	6986
QY	3900	CGAACAAATTCAAACAGAAAGCAATCGGGTTGTGCAAAACAGCCACCAAGACGGAGGC	3959
Db	6987	CGAACAAATTCAAACAGAAAGCAATCGGGTTGTGCAAAACAGCCACCAAGACGGAGGC	7046
QY	3960	TGCTGCTCCCGTGGATCCAAAGTGGCGGACCTTCGAAGCCTTCTGGCGGAACATAT	4019
Db	7047	TGCTGCTCCCGTGGATCCAAAGTGGCGGACCTTCGAAGCCTTCTGGCGGAACATAT	7106
QY	4020	GTGGAATTTTCATCAGCGGGATACAAATATTAGCAGGCTGTCCACTCTGCTGGCAACCC	4079
Db	7107	GTGGAATTTTCATCAGCGGGATACAAATATTAGCAGGCTGTCCACTCTGCTGGCAACCC	7166
QY	4080	CGCGATAGCATCATCATGGCATTCACAGCCTCTATCACAGCCCGCTCACCCACCAACA	4139
Db	7167	CGCGATAGCATCATCATGGCATTCACAGCCTCTATCACAGCCCGCTCACCCACCAACA	7226
QY	4140	TACCTCTCTGTTTAAACATCTGTGGGGGATGGGTGGCGGCCAACTTGTCTTCCAGGCG	4199
Db	7227	TACCTCTCTGTTTAAACATCTGTGGGGGATGGGTGGCGGCCAACTTGTCTTCCAGGCG	7286
QY	4200	TGCTTCTGCTTTTCGTAGGCGCGGGATCGCTGGAGGGCTGTGTGCACATAGGCTTGG	4259
Db	7287	TGCTTCTGCTTTTCGTAGGCGCGGGATCGCTGGAGGGCTGTGTGCACATAGGCTTGG	7346

QY	4260	GAAGGTGCTGTGGATATTTTGGCAGGTATTATGGACAGGGGTGGCAGCGCGCTCGTGCC	4319
DB	7347	GAAGGTGCTGTGGATATTTTGGCAGGTATTATGGACAGGGGTGGCAGCGCGCTCGTGCC	7406
QY	4320	CTTTAAGGTCATGAGCGGCGATGCCCTCCACCGAGACCTGGCTAACCTTACTCCCTGC	4379
DB	7407	CTTTAAGGTCATGAGCGGCGAGTGCCTCTCCACCGAGACCTGGTTAACTTACTCCCTGC	7466
QY	4380	TATCCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTGCGCAGCATCTACGCTCGCGCA	4439
DB	7467	TATCCTCTCCCTGGGGCCCTAGTCTGGGGTCTGTGCGCAGCATCTACGCTCGCGCA	7526
QY	4440	CGTGGGCCACAGGGAGGGGCTGTGCTAGTGGATGAACCGGCTGATAGCTTTCGCTTCGCG	4499
DB	7527	CGTGGGCCACAGGGAGGGGCTGTGCTAGTGGATGAACCGGCTGATAGCTTTCGCTTCGCG	7586
QY	4500	GGGTAAACACGCTCTCCGCCACGCACTATGCTGTGAGCGACGCTGAGCAAGTGTCAAC	4559
DB	7587	GGGTAAACACGCTCTCCGCCACGCACTATGCTGTGAGCGACGCTGAGCAAGTGTCAAC	7646
QY	4560	TCAGATCTCTCTAGTCTTACATCACTACGCTGCTGAAGAGGCTTCCACAGTGGATCAA	4619
DB	7647	TCAGATCTCTCTAGTCTTACATCACTACGCTGCTGAAGAGGCTTCCACAGTGGATCAA	7706
QY	4620	CGAGGACTGCTCCAGCGCATGCTCCGGCTAGAGATGTTTGGATTTGGATATG	4679
DB	7707	CGAGGACTGCTCCAGCGCATGCTCCGGCTAGAGATGTTTGGATTTGGATATG	7766
QY	4680	CACGGTGTGACTGATTTCAAGACTGCTCAGTCCAGTCCAAAGTTCGCGGGCAGCGCATCAT	4739
DB	7767	CACGGTGTGACTGATTTCAAGACTGCTCAGTCCAAAGTTCGCGGGCAGCGCATCAT	7826
QY	4740	AGTCCCTCTCTCATGTCAAGCTGGGTACAGGGAGTCTGGCGGGGCGACCGCATCAT	4799
DB	7827	AGTCCCTCTCTCATGTCAAGCTGGGTACAGGGAGTCTGGCGGGGCGACCGCATCAT	7886
QY	4800	GCAACACACTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAAGTTTCCATGAG	4859
DB	7887	GCAACACACTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAAGTTTCCATGAG	7946
QY	4860	GATCGTGGGCTTAGGACCTGTAGTAACAGTGGCATGGAAATTCCTCCCATTAACCGCTA	4919
DB	7947	GATCGTGGGCTTAGGACCTGTAGTAACAGTGGCATGGAAATTCCTCCCATTAACCGCTA	8006
QY	4920	CACCACGGGCCCTGCACGCGCTCCCGCGCCAAATTTCTTAGGGCGCTGTGGCGGT	4979
DB	8007	CACCACGGGCCCTGCACGCGCTCCCGCGCCAAATTTCTTAGGGCGCTGTGGCGGT	8066
QY	4980	GGCTGTGAGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTAGTCACGGGCAT	5039
DB	8067	AGGTGCTGAGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTAGTCACGGGCAT	8126
QY	5040	GACCACATGACAAAGTAAAGTCCCGTGTGAGTTCGGGCCCGGAAATTCCTTACAGAGT	5099
DB	8127	GACCACTGACAAAGTAAAGTCCCGTGTGAGTTCGGGCCCGGAAATTCCTTACAGAGT	8186
QY	5100	GGATGGGGTTCGCTGTGACAGATGACGCTCAGCGTGCAAACCCCTTCTACGGGAGGAGT	5159
DB	8187	GGATGGGGTTCGCTGTGACAGATGACGCTCAGCGTGCAAACCCCTTCTACGGGAGGAGT	8246
QY	5160	CACATTCCTGGTTCGGCTCAATCAATCTGGTGGGTACAGCTCCCATTCGAGCCCGA	5219
DB	8247	CACATTCCTGGTTCGGCTCAATCAATCTGGTGGGTACAGCTCCCATTCGAGCCCGA	8306
QY	5220	ACCGGAGTACAGTGTCTCACTTCCATGCTACCGACCCCTCCCATTCGAGCCCGA	5279
DB	8307	ACCGGAGTACAGTGTCTCACTTCCATGCTACCGACCCCTCCCATTCGAGCCCGA	8366
QY	5280	GGCTAAGCGTACGCTGGCCAGGGGATCTCCCGCTTTCGCGAGCTCATCAGTAGCCA	5339
DB	8367	GGCTAAGCGTACGCTGGCCAGGGGATCTCCCGCTTTCGCGAGCTCATCAGTAGCCA	8426
QY	5340	CGTGTCTGCGCTTCTTTGAAGGGCAACATGCACTACCGGTATGACTCCCCCGGACGTGA	5399

8427	Db		8427	CGTCTGCGCCCTTCTTGAGGACACATGCACTACCCGTCATGACTCCCGGACGCTGA	8486
5400	Qy		5400	CCTCATCGAGGCAACCTCTCTGCGCGGAGAGATGGCGGGAACATCACCCCGGTGGA	5459
8487	Db		8487	CCTCATCGAGGCAACCTCTCTGCGCGGAGAGATGGCGGGAACATCACCCCGGTGGA	8546
5460	Qy		5460	GTGAGAAATAGGTTAGTAAATTTTGACACTCTTTCGAGCCGCTCCRAAGCGGAGAGATGA	5519
8547	Db		8547	GTGAGAAATAGGTTAGTAAATTTTGACACTCTTTCGAGCCGCTCCRAAGCGGAGAGATGA	8606
5520	Qy		5520	GAGGGAAGTATCCGTTCCGCGGAGATCTCTGCGAGAGTCCAGGAAATTCCTTCGAGCGAT	5579
8607	Db		8607	GAGGGAAGTATCCGTTCCGCGGAGATCTCTGCGAGAGTCCAGGAAATTCCTTCGAGCGAT	8666
5580	Qy		5580	GCCCATATGGGCAAGCGCCGAGATTCAACCTCCCTCACTGTTAGAGTCTCTGGAAGACCCGGA	5639
8667	Db		8667	GCCCATATGGGCAAGCGCCGAGATTCAACCTCCCTCACTGTTAGAGTCTCTGGAAGACCCGGA	8726
5640	Qy		5640	CTAGCTCCCTCCAGTGTGACAGGGGTGTCATTTGCCGCTGCCAAGGCCCTCCGATACC	5699
8727	Db		8727	CTAGCTCCCTCCAGTGTGACAGGGGTGTCATTTGCCGCTGCCAAGGCCCTCCGATACC	8786
5700	Qy		5700	ACCTCCACGAGGAAGAGACGGTTGCTCTGTGAGAAATCTACCGTCTCTTCTGCCCTTGGC	5759
8787	Db		8787	ACCTTCACGAGGAAGAGACGGTTGCTCTGTGAGAAATCTACCGTCTCTTCTGCCCTTGGC	8846
5760	Qy		5760	GGAGCTCGCCCAAAAGACCTTTGGCAGCTCCGAATGCTGCGGCGTGCACAGCGGCACGGC	5819
8847	Db		8847	GGAGCTCGCCCAACAGACCTTTGGCAGCTCCGAATGCTGCGGCGTGCACAGCGGCACGGC	8906
5820	Qy		5820	AACGGCTCTCTGACACGCTCCGACAGCGGCGAGCGGGATCCGAGTTCAGTTCGTA	5879
8907	Db		8907	AACGGCTCTCTGACACGCTCCGACAGCGGCGAGCGGGATCCGAGTTCAGTTCGTA	8966
5880	Qy		5880	CTCTCTCAATGCCCCCTTGAGGGGAGCCCGGGGATCCCGATCTCAGCGACGGGTCTTG	5939
8967	Db		8967	CTCTCTCAATGCCCCCTTGAGGGGAGCCCGGGGATCCCGATCTCAGCGACGGGTCTTG	9026
5940	Qy		5940	GTCTACCGTAAGCGAGGAGGCTAGTAGGACGTCGTCTGTCTGTCGATGCTTACACATG	5999
9027	Db		9027	GTCTACCGTAAGCGAGGAGGCTAGTAGGACGTCGTCTGTCTGTCGATGCTTACACATG	9086
6000	Qy		6000	GACAGGCGCTGTATCAGCCATCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACT	6059
9087	Db		9087	GACAGGCGCTGTATCAGCCATCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACT	9146
6060	Qy		6060	GAGCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTCAAACTCTCGCAGCGAAG	6119
9147	Db		9147	GAGCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTCAAACTCTCGCAGCGAAG	9206
6120	Qy		6120	CCTGCGGAGAGAAAGGTCATCTTTGACAGACTGGAGTCTTGAGACGACCACTACCGGGA	6179
9207	Db		9207	CCTGCGGAGAGAAAGGTCATCTTTGACAGACTGGAGTCTTGAGACGACCACTACCGGGA	9266
6180	Qy		6180	CGTGTCTAAGGAGATGAGGCGAAGCGGTCCACAGTTAAGCTTAACTTCTATCCGTGGA	6239
9267	Db		9267	CGTGTCTAAGGAGATGAGGCGAAGCGGTCCACAGTTAAGGCTTAACTTCTATCCGTGGA	9326
6240	Qy		6240	GGAAGCCTGTAAGCTGACGCCCCCACTTCGSCCAGATCTTAAATTTGGCTATGGGGAAA	6299
9327	Db		9327	GGAAGCCTGTAAGCTGACGCCCCCACTTCGSCCAGATCTTAAATTTGGCTATGGGGAAA	9386
6300	Qy		6300	GGAAGCCTGTAAGCTGACGCCCGTTAAACCATCCGCTCCGTTGTCGAAGGACTT	6359
9387	Db		9387	GGAAGCCTGTAAGCTGACGCCCGTTAAACCATCCGCTCCGTTGTCGAAGGACTT	9446
6360	Qy		6360	GCTGGAAGACACTGACAGACCAATTTGACACCACTCATGTCGCAAAATATGAGTTTCTG	6419
9447	Db		9447	GCTGGAAGACACTGACAGACCAATTTGACACCACTCATGTCGCAAAATATGAGTTTCTG	9506
6420	Qy		6420	CGTCCAAACAGAGAGGGGGCGCAAGCGCTCGCTTATTCGTATTTCCAGATTTGGG	6479

QY	7560	CAACTGGGCGAGTAA	GAGCAACAGCTCA	AACTCACTCCGAGT	CGCGTCCAGTTGA	7619
Db	10647	CAACTGGGCGAGTAA	GAGCAACAGCTCA	AACTCACTCCGAGT	CGCGTCCAGTTGA	10706
QY	7620	TTTATCCAGCTGGT	TCGTCTGGTTAC	AGCGGGGAGACA	TATATCACAGCTCTCTCG	7679
Db	10707	TTTATCCAGCTGGT	TCGTCTGGTTAC	AGCGGGGAGACA	TATATCACAGCTCTCTCG	10766
QY	7680	TGCCGACCCCGCT	TGGTTCATGTGGT	GCCTACTCTCTACT	TTCTGTAGGGGTAGGCATCTA	7739
Db	10767	TGCCGACCCCGCT	TGGTTCATGTGGT	GCCTACTCTCTACT	TTCTGTAGGGGTAGGCATCTA	10826
QY	7740	TCCTACTCCCAAC	CGGATGAACGGG	GAGCTAAACAT	TCCAGGCCAATAGGCCATCTCTGTTT	7799
Db	10827	TCCTACTCCCAAC	CGGATGAACGGG	GAGCTAAACAT	TCCAGGCCAATAGGCCATCTCTGTTT	10886
QY	7800	TTTTTCCTTTTTTT	TTTTTTTTTTTTTT	TTTTTTTTTTTTTT	TTTTTTTTTTTTTTCTCCCTTT	7859
Db	10887	TTTTTCCTTTTTTT	TTTTTTTTTTTTTT	TTTTTTTTTTTTTT	TTTTTTTTTTTTTTCTCCCTTT	10946
QY	7860	TTTTTTCCTTTTTT	TCTTTCTTTCTTT	TCTTTGGTGGCT	TCCATCTTAGCCCTAGTCACGG	7919
Db	10947	TTTTTTCCTTTTTT	TCTTTCTTTCTTT	TCTTTGGTGGCT	TCCATCTTAGCCCTAGTCACGG	11006
QY	7920	CTAGCTGTGAAGG	TCGCGAGCCGCT	GACTGAGAGAGT	GCTGATACTGGCCTCTCTG	7979
Db	11007	CTAGCTGTGAAGG	TCGCGAGCCGCT	GACTGAGAGAGT	GCTGATACTGGCCTCTCTG	11066
QY	7980	CAGATCAAGT	7989			
Db	11067	CAGATCAAGT	11076			

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RESULT 12
US-09-014-416-4
; Sequence 4, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Buhk, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014, 416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 9595
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-4

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Query Match	66.5%;	Score 5312;	DB 3;	Length 9595;
Best Local Similarity	91.3%;	Pred. No. 0;		
Matches 5550; Conservative	0;	Mismatches 530;	Indels 10;	Gaps 1;
QY	1800	CATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCAC	1859	
Db	3416	CTTGGGCCCATCAGCGCCTACTCCCAACAAACGCGGGGGCGTACTTGGTTGCATCATCAC	3475	
QY	1860	TAGCCTCACAGGCGGGGACAGAAACCAAGTTCGAGGGGGAGGTCCAGGTGTCCTCCACGC	1919	
Db	3476	TAGCCTCACAGGCGGGGACAGAACCAAGTTCGAAGGGGAGGTTCAAATGCGTTTCTACCGC	3535	
QY	1920	AACAACATCTTTCTCTGGGCACCTGCGTCAATGCGCGTGTGTGGACGTCTATCATGGTGC	1979	
Db	3536	AACAACATCTTTCTCTGGGCACCTGCATCAACGCGCGTGTCTGGACGTCTTACCATGGCGC	3595	

QY	1980	CGGCTCAAGACCCCTTGGCGGCCAAAGGGGCCAATCACCCAAATGTACACAAATGTGCA	2039
DB	3596	TGGCTCGAAGACCCCTAGCCGCTCCAAAGGTCGAATCACCCCAATGTACACAAATGTAGA	3655
QY	2040	CCAGAGACCTCGTCGGCTGGCAAGCGCCCCCGGGCGCGTTCTTGTGACACCATCACCGT	2099
DB	3656	CGTGACCTCGTTCGGCTGGCAGGGCGCCCCCGGGCGCGCTCCATGACACCATGACGCTG	3715
QY	2100	CGGCAAGCTCGGACCTTTACTTTGCTCAGAGGCAATCCGATGTCTAATTCGGTGCGCCGGG	2159
DB	3716	TGGCAAGCTCGGACCTTTACTTTGGTCAAGAGACATGCTGATGTCTAATTCGGTGCGCCGGG	3775
QY	2160	GGGCGACAGCAGGGGAGCCTACTCTCCCCAGCGCCGCTCTCTTACTTTGAAGGCTCTCTC	2219
DB	3776	AGGCGACAGCAGGGGAGCTTACTCTCCCCAGCGCCGCTCTCTTACTTGAAGGCTCTCTC	3835
QY	2220	GGGCGGTCCACTGCTCTGCCCCCTGGGGCAAGCTGTGGGCATCTTTCCGGCTGCCTGTG	2279
DB	3836	GGGTGGTCCATTGTCTTGTTCCTTCGGGGCAAGCTGTGGGGCTCTTCCGGCTGCTGTGTG	3895
QY	2280	CACCCGAGGGGTGCGAAGGGCGGTGGACTTTGTATCCCTGCTAGCTCTATGAAACCATAT	2339
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QY	2340	CGGTCCTCCGCTCTTCCAGCAACTCGTCTCCCTCCGGCGGTACCGCAGACATTCAGGT	2399
DB	3956	CGGTCCTCCGCTCTTCCAGCAACTCAACCCCGGGCTGTACCGCAGACATTCAGGT	4015
QY	2400	GGCCCATCTACAGCCCTTACTGTGTAGCGGAAGACATTAAGGTCCGGCTCGGTATGC	2459
DB	4016	GGCACATCTGCACGCTCTTACTGGCAGCGCAAGAGCACCAAGTCCGGCTCGGTATGC	4075
QY	2460	AGGCCAAAGGCTATAAGTGTCTGCTGAACCGTCCGTCGCCCAACCTAGGTTCGG	2519
DB	4076	AGGCCAAGGCTAAGAGTGTCTGCTGAACCGTCCGTCGCCCAACCTAGGTTCGG	4135
QY	2520	GGGCTATATCTTAAGGCAATGCTATCGACCTTAACATCAGAACCGGGTAGGACCAT	2579
DB	4136	GGGCTATATCTTCCAGGCACACGGTATCGACCTTAACATCAGAACCTGGGGTAGGACCAT	4195
QY	2580	CACGACGGGTGCCCCCATCAGCTACTCCAATTGCAAGTTCTTTGCCGACGGTGTG	2639
DB	4196	TACCACGGGCGGCTCCATTACGTACTCCACCTATGGCAAGTTCTTTGCCGACGGTGTG	4255
QY	2640	CTCTGGGGCGCTATGACATCATATATGTGATGATGTCCTCACTGATCTGACCAAC	2699
DB	4256	TTCTGGGGCGCCTATGACATCATATATGTGATGATGTCCTCACTGATCTGACCTAC	4315
QY	2700	TATCTTGGGCATCGGCACAGTCTCTGGACCAAGGAGACGGCTGGAGCGGACTCGTCTG	2759
DB	4316	CATCTTTGGGCATCGGCACAGTCTCTGGACCAAGGAGACGGCTGGAGCGGCTCGTCTG	4375
QY	2760	GCTCGCACGGCTACGCCCTCCGGATTCGGTCACTGTCGCAATCAAAACATCGAGGAGT	2819
DB	4376	GCTCGCACCGCTACACCTCCGGGATTCGGTACCGTGCACACCCCAATATCGAGGAAT	4435
QY	2820	GGTCTGTCCAGCCTGGAGAAATCCCTTTTATGGCAAGGCATCCCCATCGAGACCAT	2879
DB	4436	AGGCTGTCCAAATGGAGAGATCCCTTTTATGGCAAGGCATCCCCATCGAGGACCAT	4495
QY	2880	CAAGGGGGGAGGCACCTCATTTTCTGCAATCCAAAGAGAAATGTGATGAGCTCGCCG	2939
DB	4496	CAAGGGGGGAGGCATCTCATTTTCTGCCATTCGAGAGAAATGTGAGGAGCTCGCCG	4555
QY	2940	GAAAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGCCCTTGATGATCCGT	2999
DB	4556	AAAGGTGACAGGCCCTTCGAGCTGAACGCTGTAGCATATTAACGGGGCCCTTGATGATCCGT	4615
QY	3000	CATACCAACTAGCGAGAGCTCATTTGCTGTAGCAACGAGCCTCTAATGACGGCTTTAC	3059
DB	4616	CATAACGCTATCGAGAGCTGTTGTGCTGGCAACAGCCTCTAATGACGGCTTTAC	4675

QY	7440	TTATGCTCAGGAACTTGGGGTACCGCCCTTCCGAGTCTGGAGACATCGGGCCAGAAG	7499
Db	9056	TTATGCTCAGGAACTTGGGGTACCGCCCTTCCGAGTCTGGAGACATCGGGCCAGAAG	9115
QY	7500	TGTCGGCGCTAGGCTACTGCTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTT	7559
Db	9116	TGTCGGCGCTAAGCTACTGCTCCAGGGGGGAGGGCGCCACTTGTGGCAGATACCTCTT	9175
QY	7560	CAACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTGCCAGTTGGA	7619
Db	9176	TAACTGGGCACTAAGGACCAAGCTTAAACTCACTCCAAATCCCGGCTGCTGCCAGTTGGA	9235
QY	7620	TTATFCAAGCTGTTGCTGCTGCTTACAGGGGGGAGACATATATACAGCCTGCTCG	7679
Db	9236	CTTGTCTGGCTGTTGCTGCTGCTTACAGGGGGGAGACATATATACAGCCTGCTCG	9295
QY	7680	TGCCCGACCCCGCTGTTTCATGTGCTACTCTCTACTCTTCTGTAGGGTAGGCATCTA	7739
Db	9296	TGCCCGACCCCGCTGTTTCATGTGCTACTCTCTACTCTTCTGTAGGGTAGGCATCTA	9355
QY	7740	TCTACTCCCAACCGATGAACGGGAGCTAAACATCCAGGGCCAAATAGGCCATCTCTGTT	7799
Db	9356	CCTGCTCCCAACCGATGAACGGGAGCTAAACATCCAGGGCCAAATAGGCCATCTCTGTT	9405
QY	7800	TTTTTCCCTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCTTT	7859
Db	9406	ATTTCTCTTTCTCT	9465
QY	7860	TTTTTTCCTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCT	7919
Db	9466	TCTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCT	9525
QY	7920	CTAGCTGTGAAGTCCGCTGAGCCGCTTCACTGCGAGAGTGTGATATCTGGCCTCTCTG	7979
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; Sequence 31, Application US/08324977			
; Patent No. 5747339			
; GENERAL INFORMATION:			
; APPLICANT: OKAYAMA, Hiroto			
; APPLICANT: FUKU, Isao			
; APPLICANT: MORI, Chisato			
; APPLICANT: TAKAMIZAWA, Akahisa			
; APPLICANT: YOSHIDA, Iwao			
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC			
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE			
; NUMBER OF SEQUENCES: 50			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Armstrong, Westerman, Hattori, McLeLland &			
; ADDRESSEE: Naughton			
; STREET: 1725 K St. N.W. Suite 1000			
; CITY: Washington			
; STATE: D.C.			
; COUNTRY: U.S.A.			
; ZIP: 20006			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0			
; SOFTWARE: ASCII			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/324,977			
; FILING DATE: 18-OCT-1994			
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; APPLICATION NUMBER: JP 2-167466			
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; APPLICATION NUMBER: JP 2-230921			
; FILING DATE: 31-AUG-1990			
; PRIOR APPLICATION DATA:			
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; FILING DATE: 09-NOV-1990			
; PRIOR APPLICATION DATA:			
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; FILING DATE: 30-JUL-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/769,996			
; FILING DATE: 02-OCT-1991			
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; APPLICATION NUMBER: US 07/635,451			
; FILING DATE: 28-DEC-1990			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Stevens-Smith, Theresa M.			
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; INFORMATION FOR SEQ ID NO: 31:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 7917 base pairs			
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Best Local Similarity 91.8%; Pred. No. 0;			
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;			
QY	1800	CATGGCGCTATTACGGCCCTACTCCCAACAGACGGCGGCTACTTTGGCTGCATCATCAC	1859
Db	1908	CTCGCGCCCATCACGGCCCTACTCCCAACAGACGGCGGCTACTTTGGCTGCATCATCAC	1967
QY	1860	TAGCCTTCACAGCGCGGACAGGAACCAAGTCCAGGGGGAGGTCCAGGTGTTCCACCGC	1919
Db	1968	TAGCCTTCACAGCGCGGACAGGAACCAAGTCCAGGGGGAGGTCCAGGTGTTCCACCGC	2027
QY	1920	AACACAATCTTCTCGGCGACCTGCTCAATGCGGTGTGTGGACTGTCTATCATGTGC	1979
Db	2028	AACACAATCTTCTCGGCGACCTGCTCAATGCGGTGTGTGGACTGTCTATCATGTGC	2087
QY	1980	CGGCTCAAGACCCCTTGGCGGCGCCAAAGGCGCCCAATCACCCAAATGTACACCAATGTGA	2039
Db	2088	TGGCTCAAGACCCCTTGGCGGCGCCAAAGGCGCCCAATCACCCAAATGTACACCAATGTGA	2147
QY	2040	CCAGGACCTGCTGCTGGCAACGCGCCCGGGGCGGCTTCTTGCACCATGACCTG	2099
Db	2148	CCAGGACCTGCTGCTGGCAACGCGCCCGGGGCGGCTTCTTGCACCATGACCTG	2207
QY	2100	CGGCGCTCGGACCTTTTACTTGTGTACAGAGGATGCGGATGTCAATCCCGGTGCGCGCGC	2159
Db	2208	TGGAGCTCAGACCTTTACTTGTGTACAGAGATGCTGACGTCAATCCCGGTGCGCGCGC	2267
QY	2160	GGGCGACAGCAGGGGAGGCTTCTTCCCGGCGGCTCTCTTGAAGGGCTCTTC	2219
Db	2268	GGGCGACAGTGGGGGAGGCTTCTTCCCGGCGGCTCTCTTGAAGGGCTCTTC	2327
QY	2220	GGGCGGTCCACTGCTCTGCCCTCGGGGCGGCTGTGGGCATCTTTCCGGGTGCGCGGTG	2279

Db	2328	GGGTGTCACAGCTCTCTGCCCCCTTCCGGCAGCGCTGTGGCACTCTTCGGGCTGCCGTATG	2387	3408	TGCTTGTTACGAGCTCACCCCCCGGCGAGACCTCGTGTAGGTTTGGGGCTTACCTGTGAACAC	3467
QY	2280	CACCCGAGGGTTGGCAAGCGGTGACCTTTGTATCCCGTTCGAGTCTATGGAAACCACTAT	2339	3360	ACCAGGGTTGCCCGTCTGCGCAGGACCATCTGAGGTTCTGGGAGAGCGTCTTTTACAGGCCCT	3419
Db	2388	CACCCGGGGGTTGGCAAGCGGTGAGCTTTGTGCCCGTAGAGTCCATGGAACTACTAT	2447	3468	ACCAGGGTTGCCCGTGTGCGCAGGACCACTGAGGTTCTGGGAGAGTGTCTTACAGGCCCT	3527
QY	2340	GGGGTCCCCGGTCTTTCACGCAAACTCGTCCCTCCGGCCGTACCGCAGACATCCAGGT	2399	3420	CACCCATAGATGACACTTCTGTCCAGACCAAGCAGGAGGAGCAACTTCCCTTA	3479
Db	2448	GGGTCTCCGGTCTTTCACGCAAACTCATCCCGCCCGCGTACCGCAGTCAATTCAGGT	2507	3528	CACCCATAGATGACACTTCTGTCCAGACCAAGCAGGAGGAGCAACTTCCCTTA	3587
QY	2400	GGCCCATCTACAGGCCCTTCTGTTAGCGGCAAGAGCACTAAGTGCCCGCTGCGTATGC	2459	3480	CCTGTAGCATACAGGCTACGTTGTGCGCAGGCGTCAAGGCTCACTCCATCTGTTGGGA	3539
Db	2508	GGCCCACTTACAGCTCCCACTGGCAGCGGCAAGAGTACTAAGTGCCCGCTGCGTATGC	2567	3588	CCTGTAGCATACAGGCTACGTTGTGCGCAGGCGTCAAGGCTCACTCCATCTGTTGGGA	3647
QY	2460	AGCCCAAGGGTATAGGTGCTTCTGCTGACCCGCTCGTCCCGCCGACCTTAGGTTTCGG	2519	3540	CCAAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGACAGGCTGACAGGCGCAACGCCCTGCT	3599
Db	2568	AGCCCAAGGGTACAAGGTGCTGCTCCTCAATCCGTCCGTGCGCTACCTTAGGTTTCGG	2627	3648	TCAAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGACAGGCTGACAGGCGCAACGCCCTGCT	3707
QY	2520	GGCGTATATGCTTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAAGACCAT	2579	3600	GTATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACACCCCATAAACAAATACAT	3659
Db	2628	GGCGTATATGCTTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAAGACCAT	2687	3708	GTACAGGCTGGAGCCGTTCCAGAAATGAGGTCAACCTCACCCACCCATTAACCAATATACAT	3767
QY	2580	CACCAAGGGTCCCCCATACAGTACTCCACCTATGCGCAAGTTTCTTGCAGCGGTGGTTG	2639	3660	CATGSCATGCATGTCGGCTGACCTGAGGTCGTCAAGAGCACCTGGGTGCTGGTAGGCGG	3719
Db	2688	TACCACAGGCGCCCCGTCACTATCTACCTATGCGCAAGTTTCTTGCAGCGGTGGTTG	2747	3768	CATGSCATGCATGTCGGCTGACCTGAGGTCGTCAAGAGCACCTGGGTGCTGGTAGGCGG	3827
QY	2640	CTCTGGGGCGCTATGACATCATATATGATGAGTGCACCTCAACTGACTCGACAC	2699	3720	AGTCTTAGCAGCTCTGCGCGCGTATTGCTGACAAACGAGGCTGCTAGCAGCTGGGTGCTGGTAG	3779
Db	2748	CTCTGGGGCGCTATGACATCATATATGATGAGTGCACCTCAACTGACTCGACAC	2807	3828	AGTCTTAGCAGCTCTGCGCGCGTATTGCTGACAAACGAGGCTGCTAGCAGCTGGGTGCTGGTAG	3887
QY	2700	TATCTTGGGCATCGGCACAGTCTTGGACCAAGCGGAGAGCGGTGGAGCGGACTCGTGT	2759	3780	GATCATCTTGTCCGAAAGCGCGGCATCATTTCCGACAGGGAAGTCTCTTACCGGAGT	3839
Db	2808	AATCTTGGGCATCGGCACAGTCTTGGACCAAGCGGAGAGCGGTGGAGCGGACTCGTGT	2867	3888	GAATATCTTGTCCGGAGCGCGGCATTTGTTCCGACAGGAGGCTTCTCTACAGGAGT	3947
QY	2760	GCTCGCCACCGCTACGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGGT	2819	3840	CGATGAGTGAAGAGTGGGCTCACAGCTCCCTTACATCGAAACAGGAAATGCAAGTGC	3899
Db	2868	GCTCGCCACCGCTACGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGGT	2927	3948	CGATGAAATGAAGAGTGGGCTCGGCTCGCACCTCCCTTACATCGAGCAGGAAATGCAAGTGC	4007
QY	2820	GGCTCTGTCAGCACTCGGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACAT	2879	3900	CGAAATAATCAAAACAGAGGCAATCGGGTGTCTGCAAAACAGCAGCAGCAGGAGGCGG	3959
Db	2928	GGCCCTGTCTAATCTGGAGAGTCCCTTCTATGGCAAGCCATCCCATTTGAAGCAT	2987	4008	CGAGCAATCAAGCAGAAAGGGTCTGGGTACTGCAAAACAGCAGCAGCAGGAGGCGG	4067
QY	2880	CAAGGGGGGAGGACCTCTATTTCTGCTCAATTCACAAAGAAATGTGATGAGCTCGCGC	2939	3960	TGCTGTCCCGTGTGGAATCCAAAGTGGCGGACCTCGAAAGCCTTCTGGGGAAGCATAT	4019
Db	2988	CAGGGGGGAGGACCTCTATTTCTGCTCAATTCACAAAGAAATGTGATGAGCTCGCGC	3047	4068	TGCTGTCCCGTGTGGAATCCAAAGTGGCGGACCTTGGAGACATTTCTGGGGAAGCAT	4127
QY	2940	GAAGCTGTCCGGCTCGGACTCAATGTCTAGCATATTAACGGGGCTTGAATGATCCGT	2999	4020	GTGGAATTTTCATCAGCGGGATAGAAATTTTAGCAGGCTTCTCACTCTGCTGGCAAGCCC	4079
Db	3048	AAAGCTGTCCGGCTCGGACTCAATGTCTAGCATATTAACGGGGCTTGAATGATCCGT	3107	4128	GTGGAATTTTCATCAGCGGGATAGAAATTTTAGCAGGCTTATCCACTCTGCTGGGAAGCCC	4187
QY	3000	CATACCAACTAGCGGAGAGCTATGTCGTAGCAACGACGCTCTATGAGGGCTTTAC	3059	4080	CGCGATAGCATCACTGATGGCATTTACAGGCTCTATCACCAGCGCGCTCACCCACCAACA	4139
Db	3108	CATACCAACTAGCGGAGAGCTATGTCGTAGCAACGACGCTCTATGAGGGCTTTAC	3167	4188	CGCAATAGCATCACTGATGGCATTTACAGGCTCTATCACCAGCGCGCTCACCCACCAAG	4247
QY	3060	CGCGATTTTCGACTCGAGTCAATATGATGATATTAACGGGGCTTGAATGATCCGT	3119	4140	TACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGC	4199
Db	3168	GGCGGACTTTGACTCGAGTCAATATGATGATATTAACGGGGCTTGAATGATCCGT	3227	4248	TACCTCTCTGTTTAAATCTTTGGGGGGTGGGTGGCTGCGCCAACTCGCCCCCCCCAGCGC	4307
QY	3120	CCTGGACCGGACTTACCAATGAGACGACGACCGGTGCCAAGACGCGGTTCAGGCTC	3179	4200	TGCTTCTGCTTTTCGTAAGCGCGCATCGCTGAGCGGCTGTTGGAGCATATGGCTTGG	4259
Db	3228	CTTGGATCCCACTTACCAATGAGACGACGACCGGTGCCAAGACGCGGTTCAGGCTC	3287	4308	CGCTTCGGCTTTTCGTTGGGGCGCGCATCGCGGTGCGGCTGTTGGAGCATATGGCTTGG	4367
QY	3180	GACAGCGGAGGAGGAGCTGAGTGGGAGGAGTGGGCAATTTAGGTTTGTGATCCAGG	3239	4260	GAAGGTCTTGTGGATATTTTGGCAGGCTTATGGAGCAGGCGGTGGGAGGCGCGCTCGTGGC	4319
Db	3288	GACAGCGGAGGAGGAGCTGAGTGGGAGGAGTGGGCAATTTAGGTTTGTGATCCAGG	3347	4368	GAAGGTCTTGTGGATATTTTGGCGGCTTATGGAGCAGGAGTGGCGCGCGCTCGTGGC	4427
QY	3240	AGAACCGGCTCGGGCATGTTTCAATCTCTCGGTTCTGTGAGTGTATGACGCGGCTG	3299	4320	CTTTAAGGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGGTAACTACTCTCCCTGC	4379
Db	3348	AGAACCGGCTCGGGCATGTTTCAATCTCTCGGTTCTGTGAGTGTATGACGCGGCTG	3407	4428	CTTTAAGGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGGTAACTACTCTCCCTGC	4487
QY	3300	TGCTTGGTACGAGCTCAGCGCCCGCAGACCTCAGTTAGGTTGCGGGCTTACCTAAACAC	3359	4380	TATCTCTCTCCCTGCGGCTAGTGTGCGGGTGTGTCGCGAGCATCTGCGTGGCA	4439
				4488	CATCTCTCTCTCTGCGGCTTGTGTCGCGGCTGCTGTCGAGCAATACTGCTCGCA	4547

Qy	4440	CQTGGGCCAGGGAGGGGGCTGTGAGTGGATGAA	CGCGCTGTATGAGCTTCCGCTTCGGG	4499
Db	4548	CQTGGGTCGGGAGAGGGGGCTGTGAGTGGATGAA	CGCGCTGTATGAGCTTCCGCTTCGGG	4607
Qy	4500	GGGTAAACAGCTCTCCGCCACGACCTATGTGCTGAGAGGAGCGCTGACGACGCTGAC		4559
Db	4608	GGGTAAATCATGTTTCCGCCACGACCTATGTGCTGAGAGGAGCGCGCGAGCGCTGTTAC		4667
Qy	4560	TCAGATCCTCTCTAGTCTTACCACATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAA		4619
Db	4668	TCAGATCCTCTCCAGCCTTACCATCACTCAGCTGCTGAAAGGCTCCACAGTGGATTA		4727
Qy	4620	CGAGGACTGTCTCACGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATG		4679
Db	4728	TGAAGACTGTCTCCACACCGTGTTCGGCTCGTGGCTAAGGATGTTTGGGACTGGATATG		4787
Qy	4680	CACGGTGTGACTGATTTTAAGACTGTGCTCCAGTCCAAGCTCTGCGCGGATTCGCGG		4739
Db	4788	CACGGTGTGACTGACTTCAAGACTGTGCTCCAGTCCAAGCTCTGCGCGGAGCTACTCGG		4847
Qy	4740	AGTCCCTCTCTCATGTCAAGCTGGGTACAAGGAGTCTGGCGGGCGACGGCATCAT		4799
Db	4848	AGTCCCTTTTTCTGTGTCGCAACCGGGGTACAGGGAGTCTGGCGGGGAGACGGCATCAT		4907
Qy	4800	GCAAAACACCTGCCATGTGTGGAGACAGATCACGGGACATGTGTAAGAAAGTTCATGAG		4859
Db	4908	GCAAAACACCTGCCATGTGTGGAGACAGATCACGGGACATGTCAAAAGAGTTCATGAG		4967
Qy	4860	GATCGTGGGGCTAGGACTGTGTATACATGTCGATGGACATTCCTCCATTAACGCGTA		4919
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Qy	4920	CACACGGGCGCTGCAAGCTCTCCCGGGCGCAAAATTAATCTAGGGCGCTGTGGCGGT		4979
Db	5028	CACACGGGCGCTGCAAGCTCTCCCGGGCGCAAAATTAATCTAGGGCGCTGTGGCGGT		5087
Qy	4980	GGCTCTCGAGGAGTACGTGTGAGGTTACGCGGTGGGGATTCACATCGTGAAGGCGAT		5039
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Qy	5040	GACCACTGACAAAGTAAAGTGGCGTGTGAGTTCCGGCGCGCGCGCGCGCGCGCGAT		5099
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Qy	5220	ACCGAGCTGAGTGTGCTCATTTCCATGCTCACCGACCCCTCCACATTTACGGCGGAGAC		5279
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Qy	5340	GCTGTCTGGCGCTTCTTGAAGGCAACATGCACTACCGGTGATGATCTCCCGGAGCTGGA		5399
Db	5448	GTGTCTGGCGCTTCTTGAAGGCAACATGCACTACCGGTGATGATCTCTCGGAGCTGGA		5507
Qy	5400	CTTCATCGAGCCAACTCTGTGGCGCAGGAGTGTGGCGGAGACATCACCGCGTGA		5459
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Qy	5460	GTGAGAAAATAAGGTAGTAATTTTGGACTTTTCGAGCGCTCTTCAAGCGGAGGAGTGA		5519
Db	5568	GTGAGAAAATAAGGTAGTAATTTTGGACTTTTCGAGCGCTCTTTCGAGCGCTTTCGAGCTG		5627
Qy	5520	GAGGAAATATCCCTTCGGCGGAGATCCTGTGGAGGTTCAGGAAATTCCTCTCGAGCGAT		5579
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Qy	5580	GCCCATATGGGCAACGCGCGGATTAACCCCTCCACTGTAGAGTCTTGGAGGACCGCGA		5639
Db	5688	GCCCATATGGGCGCGCGGATTAACCCCTCCACTGTAGAGTCTTGGAGGACCGCGA		5747
Qy	5640	CTACGTCTCCCTCAGTGTGTACACGGGTTCCTATTCGCGCTGCCAAGGCGCTCTCCGATACC		5699
Db	5748	CTACGTCTCCCTCAGTGTGTACACGGGTTCCTATTCGCGCTGCCAAGGCGCTCTCCGATACC		5807
Qy	5700	ACCTCCACGAGGAGGAGGAGCGTGTGCTGTGAGAAATCTACCGTGTCTTCTGCTCTTAGC		5759
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Db	5868	GGAGTCTGCGCAAAAGACCTTCGGCAGCTTCGAAATCGTGGCGCTCGACAGCGGACGGC		5927
Qy	5820	AAAGCGCTCTCTGTACACCGCTCCGACGAGCGCGGACGCGCGGATCCGACGTTGAGTCTGTA		5879
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Qy	6120	CTGTGGCGAAGAGGTCACCTTTGACAGCTGAGGTCTCTGAGACCACTACCGGGA		6179
Db	6228	CTGTGGCGAAGAGGTCACCTTTGACAGCTGAGGTCTCTGAGACCACTACCGGGA		6287
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Db	6288	CGTGTCTCAAGGAGTCA		

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DB	2028	HACACAACTTTCTTGGCGACTCGGTCAACGGCGTGTGGACCGGTTTACCATGGTGC 2087
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DB	2148	CCAGGACCTGTCGGCTGCAAGCGCCCGGGGGCGCTTCTTGGACACCATGACCTG 2207
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DB	2208	TGGGACTCAGACCTTTACTTGGTACAGGAGCATGTCTGACGTCATTCGGTGGCGCGG 2267
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RESULT 15

US-08-904-686A-31

; Sequence 31, Application US/08904686A

; Patent No. 5998130

; GENERAL INFORMATION:

; APPLICANT: OKAYAMA, Hiroto

; APPLICANT: FUKU, Isao

; APPLICANT: MORI, Chisato

; APPLICANT: TAKAMIZAWA, Akahisa

; APPLICANT: YOSHIDA, Iwao

; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Armstrong, Westerman, Hattori, McLeand &

; STREET: 1725 K St. N.W. Suite 1000

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,686A
; FILING DATE: 01-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/324,977
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,706
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: McLeiland, Le-Nhung
; REGISTRATION NUMBER: 31,541
; REFERENCE/DOCKET NUMBER: 900703G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7917 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA from genomic RNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7862
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..7916
; OTHER INFORMATION: /note= "sequence = 1500 - 9416 of
; OTHER INFORMATION: SEQ ID NO: 1"
; US-08-904-686A-31

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Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;

QY 1800 CATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCAC 1859
DB 1908 CCTCGCGCCCATCACGCCTACTCCCAACAGACGCGGCGCCTACTTGGTTGCATCATCAC 1967

QY 1860 TAGCCTCAGCGCGGACAGGAACAGGTCGAGGGGAGGTCCAGGTGCTCTCCACCCG 1919
DB 1968 TAGCCTTACAGGCGGACCAAGAACAGGTCGAGGGGAGGTTCAGGTGTTTCCACCCG 2027

QY 1920 AACACAATCTTCTCGGCGCCTGCTCAATGCGGTGTTGGACTGTCTATCATGGTGC 1979
DB 2028 AACACAATCTTCTCGGCGCCTGCTCAATGCGGTGTTGGACTGTCTATCATGGTGC 2087

QY 1980 CGGCTCAAGACCTTTCGCGGCGCCAAAGGCGCCAAATCACCCAAATGTACACCAATGTGGA 2039
DB 2088 TGGCTCAAGACCTTTCGCGGCGCCAAAGGCGCCAAATCACCCAAATGTACACCAATGTGGA 2147

QY 2040 CCAGGACCTCTGCGGTGGGAAGAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACCTG 2099

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DB 2148 CCAGGACCTCTGCGGTGGCCCAAGCCCCCGGGCGCGTTCCTTGACACCATGCACCTG 2207
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QY 2220 GGGCGGTCCACTGCTCTGCCCCCTCGGGGACACCTGTGGGATCTTTGGGGCTTCGGTGG 2279
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Db	3528	CACCAATAGAGCGGCAATTTCTGTCCAGATTAAGCAGGAGGAGCACTTCCCTTA	3587	Qy	4560	TCAGATCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGGCTTCCACAGTGGATCA	4619
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Mon Aug 16 09:32:31 2004

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Search completed: August 12, 2004, 13:05:06
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 02:14:50 ; Search time 19689 Seconds
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Title: US-10-005-469-4

Perfect score: 7992

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pl:

9: gb_pr:

10: gb_ro:

11: gb_sts:

12: gb_sy:

13: gb_un:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

20: em_om:

21: em_or:

22: em_ov:

23: em_pat:

24: em_ph:

25: em_pl:

26: em_ro:

27: em_sts:

28: em_un:

29: em_vi:

30: em_htg_hum:

31: em_htg_inv:

32: em_htg_other:

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41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	7982.6	99.9	7989	6	AR406043	AR406043 Sequence
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8	7943	99.4	8001	6	AR406047	AR406047 Sequence
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ALIGNMENTS

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LOCUS

DEFINITION

AX739972

Accession

AX739972

Version

AX739972.1

Keywords

Source

Organism

Reference

Authors

Title

Journal

Sequence 3 from Patent WO02059321.
GI:30519246

linear PAT 08-MAY-2003

unidentified
unidentified
unclassified.

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de Francesco R., Migliaccio, G. and Paonessa G.
Hepatitis C virus replicons and replicon enhanced cells
Patent: WO 02059321-A 3 01-AUG-2002;
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2701 ATCTGGGCAATCGGCAAGCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTGCTGCTG 2760
2701 ATCTGGGCAATCGGCAAGCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTGCTGCTG 2760
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2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTATGGCAAGGCCATCCCCATCGAGACCATC 2880
2881 AAGGGGGGAGGACCTCATTTCTGCGCATTCGAAGAAATGTGATGAGCTCGCGCG 2940
2881 AAGGGGGGAGGACCTCATTTCTGCGCATTCGAAGAAATGTGATGAGCTCGCGCG 2940
2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGCTTGTATCGGTC 3000
2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGCTTGTATCGGTC 3000
3001 ATACCAACTAGCGGAGAGCTCATTTGTGTAGCAACGAGCTCTTAATGAGCGCTTTACC 3060
3001 ATACCAACTAGCGGAGAGCTCATTTGTGTAGCAACGAGCTCTTAATGAGCGCTTTACC 3060
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3061 GCGGATTCGACTCAATGATGCAATCATGTGTACCCAGACAGTTCGACTTCAGC 3120
3121 CTGGACCCGACCTTCACTTGGAGACGACGACCGTGCCCAAGAGCGGTGTCAAGCTCG 3180
3121 CTGGACCCGACCTTCACTTGGAGACGACGACCGTGCCCAAGAGCGGTGTCAAGCTCG 3180
3181 CAGCGCGGAGGACGACCTGAGTGGGAGGAGTGGGCAATTTACAGGTTTGTGATCAAG 3240
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3361 CCAGGTTGCCCGTCTGCGAGACCAATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTC 3420
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3721 GTCTAGACCTCTGGCGGGTATGCTGCTGACAAAGGAGCGGTGCTATGTTGGGAGG 3780
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4081 GCGATAGCATCACTGATGCAATTTACAGGCTTATCAACAGCGCTCACCACCCCAAT 4140
4081 GCGATAGCATCACTGATGCAATTTACAGGCTTATCAACAGCGCTCACCACCCCAAT 4140
4141 ACCCTCTGCTTTAAATCCTGGGGGATGGGTGGCGGCCCACTTGTCTCTCCAGGCT 4200
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Db 121 CCCCTCCGGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
Qy 181 GACGACCGGGTCTTTCTTTGATCAACCCGCTCAATGCTGAGATTTGGGGGTGCCCC 240
Db 181 GACGACCGGGTCTTTCTTTGATCAACCCGCTCAATGCTGAGATTTGGGGGTGCCCC 240
Qy 241 GCGAGATGCTAGCCGAGTAGTGGTTCGGAAGGCGTTCGCTGATAGG 300
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Qy 301 GTGCTTGGAGTCCCGGGAGTCTCGTAGACCGTGCACCATGACGACGAATCCTAAAC 360
Db 301 GTGCTTGGAGTCCCGGGAGTCTCGTAGACCGTGCACCATGACGACGAATCCTAAAC 360
Qy 361 CTCAAGAAAAACCAAGAGGCGCGCATGATTGAACAAGATGGATTGACAGCAATCCTAAC 420
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Qy 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
Db 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
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Db 481 CTGATGCCCGCTGTTCGGCTGTGACGCGAGGGCGCGGTTCTTTTGTCAAGACCG 540
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Db 721 AAGTATCCATCATGGTGTGATGCAATGGCGGCTGATGAGCTTGTATCGGCTACCTGCC 780
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Db 781 CATTCGACCAACCAAGCGAATCATCGCATCGAGGAGCATCTCGATGGAAGCGGTC 840
Qy 841 TTCTCGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCCAGCGAATCTGTTCG 900
Db 841 TTCTCGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCCAGCGAATCTGTTCG 900
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Db 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTGTGGCTACCCGTGATTTGCTGAAGC 1080
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Db 1141 AGCCATCGCCTTCTATCGCCTTCTTACGAGTTCCTCTGAGTTTAAACAGACCAACG 1200
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Db 1741 AACGCTAGGCGGCGGACGAGGAGCTGCTTTTCTTTGAAAAACACGATAATACC 1800
Qy 1801 ATGGCGCTTATTACGGCTTACTCCCAAGAGCGAGGCTTCTTGGCTGATCATCACT 1860
Db 1801 ATGGCGCTTATTACGGCTTACTCCCAAGAGCGAGGCTTCTTGGCTGATCATCACT 1860
Qy 1861 AGCCTCAGAGCGGCGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
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Qy 1921 ACACATCTTCTGCGGACCTGCGTCAATGGGCTGTGTGAGTGTGTATCATGTGGC 1980
Db 1921 ACACATCTTCTGCGGACCTGCGTCAATGGGCTGTGTGAGTGTGTATCATGTGGC 1980
Qy 1981 GGCTCAAGACCTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2040
Db 1981 GGCTCAAGACCTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2040
Qy 2041 CAGGACCTGTGGCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
Db 2041 CAGGACCTGTGGCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
Qy 2101 GCGAGCTCGGACCTTTACTTGGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
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Qy 2161 GCGGACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
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Qy 2221 GCGGCTCCTGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Db 2221 GCGGCTCCTGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Qy 2281 ACCGAGGGGTTCGAGAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATG 2340
Db 2281 ACCGAGGGGTTCGAGAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATG 2340

Qy	2341	CGGTCCCGGTTCTTCA	CGGACAACTCGTCCCTCGGCCGTACGCGAGACATTC	CCAGGTG	2400
Db	2341	CGGTCCCGGTTCTTCA	CGGACAACTCGTCCCTCGGCCGTACGCGAGACATTC	CCAGGTG	2400
Qy	2401	GCCCATCTACACGCCCTTACTGGTAGCGGCAAGACACTAAGGTG	CCGGTCGGCTGCGTATGCA	2460	
Db	2401	GCCCATCTACACGCCCTTACTGGTAGCGGCAAGACACTAAGGTG	CCGGTCGGCTGCGTATGCA	2460	
Qy	2461	GCCCAAGGTTAAAGTGTCTCTCTGAAACCGTCCGTCGGCCGCCACCCCTAGGTTTC	CGGG	2520	
Db	2461	GCCCAAGGTTAAAGTGTCTCTCTGAAACCGTCCGTCGGCCGCCACCCCTAGGTTTC	CGGG	2520	
Qy	2521	GGGTATATGTCTAAGGCATAGGTATCGACCTAACATCAGAAACCGGGTAAAGACCATC	2580		
Db	2521	GGGTATATGTCTAAGGCATAGGTATCGACCTAACATCAGAAACCGGGTAAAGACCATC	2580		
Qy	2581	ACCACGGGTGCCCCCATCAGCTACTCCACTATGGCAAGTTTCTTGCGGAGGGTGTGCTG	2640		
Db	2581	ACCACGGGTGCCCCCATCAGCTACTCCACTATGGCAAGTTTCTTGCGGAGGGTGTGCTG	2640		
Qy	2641	TCTGGGGCGCCTATGACATCATTAATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700		
Db	2641	TCTGGGGCGCCTATGACATCATTAATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700		
Qy	2701	ATCTTGGGCATCGGCA	CHAGTCTCTGGACCAAGCGGAGCGCTGAGCGCGACTCGTCGTG	2760	
Db	2701	ATCTTGGGCATCGGCA	CHAGTCTCTGGACCAAGCGGAGCGCTGAGCGCGACTCGTCGTG	2760	
Qy	2761	CTCGCACCGCTACGCCCTCGGGATCCGTACCGTGCACATCCAAACATCGAGGAGGTG	2820		
Db	2761	CTCGCACCGCTACGCCCTCGGGATCCGTACCGTGCACATCCAAACATCGAGGAGGTG	2820		
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATC	2880		
Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATC	2880		
Qy	2881	AAGGGGGGAGGCACCTCATTTTCTGCCATTC	CAAGAAGAAATGTGATGAGCTCGCGCG	2940	
Db	2881	AAGGGGGGAGGCACCTCATTTTCTGCCATTC	CAAGAAGAAATGTGATGAGCTCGCGCG	2940	
Qy	2941	AAGCTGTCCGCGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGATGTATCCGTC	3000		
Db	2941	AAGCTGTCCGCGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGATGTATCCGTC	3000		
Qy	3001	ATACCAACTAGCGGAGACGTCATGTCTGTAGCAACGGACGCTCTAATGACGGCTTTACC	3060		
Db	3001	ATACCAACTAGCGGAGACGTCATGTCTGTAGCAACGGACGCTCTAATGACGGCTTTACC	3060		
Qy	3061	GGCGATTCGACTCAGTGTGCAATACATGTGTCAACCCAGACAGTGCACCTTCAGC	3120		
Db	3061	GGCGATTCGACTCAGTGTGCAATACATGTGTCAACCCAGACAGTGCACCTTCAGC	3120		
Qy	3121	CTGACCCGACCTTACCAATTGAGACGACGCGTGCACCAAGACCGGCTGTCAGCTCG	3180		
Db	3121	CTGACCCGACCTTACCAATTGAGACGACGCGTGCACCAAGACCGGCTGTCAGCTCG	3180		
Qy	3181	CAGCGCGAGGCAAGGATCGTAGGGGCAAGATGGGCATTTACAGGTTCTGTGACTCCAGCA	3240		
Db	3181	CAGCGCGAGGCAAGGATCGTAGGGGCAAGATGGGCATTTACAGGTTCTGTGACTCCAGCA	3240		
Qy	3241	GAACGGCCCTCGGGCATGTTTCGATTCCTCGTTCGTGCGAGTGTGATGACCGGGCTGT	3300		
Db	3241	GAACGGCCCTCGGGCATGTTTCGATTCCTCGTTCGTGCGAGTGTGATGACCGGGCTGT	3300		
Qy	3301	GCTTGTGTACAGCTACGCCCGCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA	3360		
Db	3301	GCTTGTGTACAGCTACGCCCGCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA	3360		
Qy	3361	CCAGGGTTCGCTCTGCGACGACCATCTGGAGTCTTGGAGAGGCTCTTACAGGCTC	3420		
Db	3361	CCAGGGTTCGCTCTGCGACGACCATCTGGAGTCTTGGAGAGGCTCTTACAGGCTC	3420		
Qy	3421	ACCACATAGACGCCCATTTTGTGCCAGACTTAAGCAGGCGAGAGACAACTTCCCTTAC	3480		

3421 ACCACATAGACGCCCATTTCTTGCCAGACTAAGCAGCAGGAGACAATCTCCCTAC 3480

3481 CTGCTAGCATACAGGCTACGGTGTGGCCAGAGGCTCAGCTCGACTCATCTCATGTGGGAC 3540

3481 CTGCTAGCATACAGGCTACGGTGTGGCCAGAGGCTCAGGCTCACCTCCATCGTGGGAC 3540

3541 CAAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGACGGGCCAAGCCCTGCTG 3600

3541 CAAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGACGGGCCAAGCCCTGCTG 3600

3601 TATAGGCTGGAGCCGTTCAACACGAGGTTACTACACACACGCCCATAAACCAATATCATC 3660

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3721 GTCTTAGCAGCTCTGGCCGGTATTCCTGTGACAAAGCAGCGCTGTGCTATTTGGGCGAG 3780

3781 ATCATTTGTCGGAAGCCGCCCATCATTTCCCGACAGGGAAGTCTTTACCGGAGTTTC 3840

3781 ATCATTTGTCGGAAGCCGCCCATCATTTCCCGACAGGGAAGTCTTTACCGGAGTTTC 3840

3841 GATGAGATGGAAGTGGGCTCAGACCTCCCTTATCATCGAAGGGAATGCAAGTCTGCC 3900

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4261 AAGGTGCTGTGGAATTTTGGCAGGTTATGGAGCAGGGGTGGAGCGGCGCTCTGGGCC 4320

4261 AAGGTGCTGTGGAATTTTGGCAGGTTATGGAGCAGGGGTGGAGCGGCGCTCTGGGCC 4320

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4441 GTGGGCCACAGGGAGGGGCTGTGAGTGAATGAACCGGCTGATAGCGTTTCGTTTCGGG 4500

4501 GGTAAACAGCTCTCCCGCAGSCATATGTGCTCAGAGGCGACGCTGAGCAGCTGCTACT 4560

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Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
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Db 7981 AGATCAAGT 7989

RESULT 3
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LOCUS AX036255 7989 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 4 from Patent EP1043399.
ACCESSION AX036255
VERSION AX036255.1 GI:11225871
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Bartenschlager, R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 4 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:11103"

ORIGIN

Query Match 99.9%; Score 7982.6; DB 6; Length 7989;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 GCCAGCCCCGATTTGGGGGCGACACTCCACATAGATCACTCCCTCTGTGAGAACTACTG 60
QY 61 TCTTTCAGCAGAAAGCGCTTAGCCATGGCTTAGTATGATGCTGCTGAGCTCCAGAC 120
Db 61 TCTTTCAGCAGAAAGCGCTTAGCCATGGCTTAGTATGATGCTGCTGAGCTCCAGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGAAATGGCAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGAAATGGCAG 180
QY 181 GAGACCGGGTCTTTCTTGGATCAACCCGCTCAATGCTTGGAGATTTGGCGCTGCCCCC 240
Db 181 GAGACCGGGTCTTTCTTGGATCAACCCGCTCAATGCTTGGAGATTTGGCGCTGCCCCC 240
QY 241 GCCAGACTGCTAGCCGAGTAGTGTGGGTGCGAAAGGCTTGTGGTACTGCTGATGAG 300
Db 241 GCCAGACTGCTAGCCGAGTAGTGTGGGTGCGAAAGGCTTGTGGTACTGCTGATGAG 300
QY 301 GTGCTTGCAGTGCCCGGGAGGTCTCGTAGACCGGTGACCGGAGGAGTTCGAGTTCCTAAC 360
Db 301 GTGCTTGCAGTGCCCGGGAGGTCTCGTAGACCGGTGACCGGAGGAGTTCGAGTTCCTAAC 360
QY 361 CTCAAAGAAAACCAAGGGCGCCCATGATTGAACAAGATGGAATGCGACGAGGTTCTC 420
Db 361 CTCAAAGAAAACCAAGGGCGCCCATGATTGAACAAGATGGAATGCGACGAGGTTCTC 420
QY 421 CGGCGCTTGGGTGGAGGGCTATTCCGGTATGACTGGGCAACAAGAAATCGGCTGT 480

Db 421 CGCGCGCTTGGGTGGAGGCTATTGCGCTATGATCGGCGACAAACAGACAATCGGTGCT 480
 Qy 481 CTGATGCGCGCTGTTCCGGCTGTGAGCGAGGGCGCGCGGTCTTTTGTCAAGACCG 540
 Db 481 CTGATGCGCGCTGTTCCGGCTGTGAGCGAGGGCGCGCGGTCTTTTGTCAAGACCG 540
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 Qy 661 TGCTATTGGGGAAGTGGCGGAGGAGGATCTCTGTGATCTGATCTGCTGCTGCTGCGAGA 720
 Db 661 TGCTATTGGGGAAGTGGCGGAGGAGGATCTCTGTGATCTGATCTGCTGCTGCTGCGAGA 720
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 Db 721 AAGTATCCATCATGCTGATGCAATGCGCGGCTGCATACGCTTGATCCGGCTACTGCG 780
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 Db 781 CATTCGACCAACAGCAACATCGCATCGAGCGACAGTACTCGGATGGAAGCGGTC 840
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 Db 841 TTGTCGATCAGGATGATCTGGAGGAAGAGATCAGGGGCTCGGCGAGCGAAGCTGTCG 900
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 Db 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
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 Qy 1441 GTTTCCTTGAAGCTTCTTGAAGCAACAAACAGTCTGTAGCGACCTTTTGCAGGAGCGG 1500
 Db 1441 GTTTCCTTGAAGCTTCTTGAAGCAACAAACAGTCTGTAGCGACCTTTTGCAGGAGCGG 1500
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 Db 1501 AACCCCCACCTGGCGAGAGTGCCTCTGCGGCGAAAGCGCAAGTATTAAGATACCT 1560

Qy 1561 GCAAAGCGGCAAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
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 Qy 1621 TGGCTCTCTCAAGGCTATTCAAAGGGGCTGAGGATGCCAGAGTACCCCATGT 1680
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 Db 2041 CAGGACTCTGCTGCGTGGCAAGCGCGCGGCGGCTTCTTGCACCATGCACTGCG 2100
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QY 4681 ACAGGTTTGAATTTCAAGACCTTGGCTCCAGTCCAGCTCTCTGCGGATTTGGCGGA 4740
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Db 7921 TAGCTGTGAAGTCCGTCGCTGAGCGCTGAGTCTGAGAGAGTCTGATCTGCTCTCTCTC 7980
QY 7981 AGATCAAGT 7989
Db 7981 AGATCAAGT 7989

RESULT 4

SSE242652

LOCUS

DEFINITION Hepatitis C virus replicon I377/NS3-3'UTR.

989 bp

RNA

linear

SYN 11-MAY-2000

ACCESSION
VERSION
KEYWORDS

AJ242652 GI:5441834
core-neo gene; NS2 gene; NS2 proteinase; NS3 gene; NS4B
proteinase/helicase; NS3/4A proteinase cofactor; NS4A gene; NS4B
gene; NS4B protein; NS5a gene; NS5a phosphoprotein; NS5b gene; NS5B
RNA dependent RNA polymerase; polyprotein.
Hepatitis C virus replicon I377/NS3-3'UTR
Hepatitis C virus replicon I377/NS3-3'UTR
artificial sequences; vectors.

SOURCE

ORGANISM

AUTHORS

REFERENCE

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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QY	1261	CGAAGCGGCTTGGATAAAGCGCGGTGTGCGTTTGTCTATATGTATTTTCCACCATATTG	1320	Db	2341	CGGTCCCAGGCTTTCACGGCAAACTCGTCCCTCGCGCCGTACCGCAGACATTCACAGGTG	2400
Db	1261	CGAAGCGGCTTGGATAAAGCGCGGTGTGCGTTTGTCTATATGTATTTTCCACCATATTG	1320	QY	2401	GCCCATCTACAGCCCTTACTGCTAGCGCAAGAGACACTAAGGTGCGCGCTGCGTATGCA	2460
QY	1321	CGGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTGACGAGCATTCCT	1380	Db	2401	GCCCATCTACAGCCCTTACTGCTAGCGCAAGAGACACTAAGGTGCGCGCTGCGTATGCA	2460
Db	1321	CGGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTGACGAGCATTCCT	1380	QY	2461	GCCCAAGGGTAAAGGTGCTGTCTCTGAAACCGGTCCGTGCGCGCCACCTAGTTTCGGG	2520
QY	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGCAATGTCTGTGAAGGAACA	1440	Db	2461	GCCCAAGGGTAAAGGTGCTGTCTCTGAAACCGGTCCGTGCGCGCCACCTAGTTTCGGG	2520
Db	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGCAATGTCTGTGAAGGAACA	1440	QY	2521	GCGTATATGTCTAAGGCACATGGTATCGACCTAAACATCAGAACCGGGGTAAAGACCATC	2580
QY	1441	GTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGCTCTGTAGCAGCCCTTTGACGCGAGGG	1500	Db	2521	GCGTATATGTCTAAGGCACATGGTATCGACCTAAACATCAGAACCGGGGTAAAGACCATC	2580
Db	1441	GTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGCTCTGTAGCAGCCCTTTGACGCGAGGG	1500	QY	2581	ACCACGGGTGCCCCCATCACGTACTCCACCTATGCAAGTTTCTTGCCGACGCTGGTTCG	2640
QY	1501	AACCCCCACCTGGCGACAGGTGCTCTGCGGCCAAAAGCCACGCTGTATAGATACACT	1560	Db	2581	ACCACGGGTGCCCCCATCACGTACTCCACCTATGCAAGTTTCTTGCCGACGCTGGTTCG	2640
Db	1501	AACCCCCACCTGGCGACAGGTGCTCTGCGGCCAAAAGCCACGCTGTATAGATACACT	1560	QY	2641	TCTGGGGCGCTATGACATCATATATGTGATGAGTGCCACTCAACTGACTCGACCACT	2700
QY	1561	GCAAGGCGGCAACACCCAGTGCCACGCTGTGTGAGTGTGGATAGTTGTGGAAAGAGTCAA	1620	Db	2641	TCTGGGGCGCTATGACATCATATATGTGATGAGTGCCACTCAACTGACTCGACCACT	2700
Db	1561	GCAAGGCGGCAACACCCAGTGCCACGCTGTGTGAGTGTGGATAGTTGTGGAAAGAGTCAA	1620	QY	2701	ATCCTGGGCATCGGCACAGTCTCTGGAACCAAGCGGAGCGGTGGAGCGCGACTCGTCGTG	2760
QY	1621	TGGCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGGATGCCAGAAAGTACCCCATTTG	1680	Db	2701	ATCCTGGGCATCGGCACAGTCTCTGGAACCAAGCGGAGCGGTGGAGCGCGACTCGTCGTG	2760
Db	1621	TGGCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGGATGCCAGAAAGTACCCCATTTG	1680	QY	2761	CTCGCCACCGCTACCGCTCCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGGTG	2820
QY	1681	ATGGGATCTGATCTGGGCTCTGGTGCAATGCTTTACATGTTTGTAGTGGAGTTTAA	1740	Db	2761	CTCGCCACCGCTACCGCTCCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGGTG	2820
Db	1681	ATGGGATCTGATCTGGGCTCTGGTGCAATGCTTTACATGTTTGTAGTGGAGTTTAA	1740	QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCCCATCGAGACCATC	2880
QY	1741	AACGTCTAGGCCCCCGAACAACCGGGACGTGTTTCTTCTTGAAGAACACGATATACC	1800	Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCCCATCGAGACCATC	2880
Db	1741	AACGTCTAGGCCCCCGAACAACCGGGACGTGTTTCTTCTTGAAGAACACGATATACC	1800	QY	2881	AAGGGGGGAGGACCTCATTTCTGCGCATCCAAAGAAATGTGATGAGCTCGCGCG	2940
QY	1801	ATGGCGCTATTACGGGCTATCTCCCAACAGAGCGGCTTACTTGGTGCATCATCACT	1860	Db	2881	AAGGGGGGAGGACCTCATTTCTGCGCATCCAAAGAAATGTGATGAGCTCGCGCG	2940
Db	1801	ATGGCGCTATTACGGGCTATCTCCCAACAGAGCGGCTTACTTGGTGCATCATCACT	1860	QY	2941	AAGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGATCCGTC	3000
QY	1861	AGCTCACAGCCGGGACAGAACAGGTCAAGGGGAGGTCCAGGTGTTCTCACCGCA	1920	Db	2941	AAGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGATCCGTC	3000
Db	1861	AGCTCACAGCCGGGACAGAACAGGTCAAGGGGAGGTCCAGGTGTTCTCACCGCA	1920	QY	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC	3060
QY	1921	ACAAATCTTTCTGGCGACTCGGTCAATCGCGGTGTGGAGTGTCTATCATGTGCC	1980	Db	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC	3060
Db	1921	ACAAATCTTTCTGGCGACTCGGTCAATCGCGGTGTGGAGTGTCTATCATGTGCC	1980	QY	3061	GGCGATTTTCGACTCAGTGATCGACTCAATACATGTGTGTCACCCAGACAGTTCGAGC	3120
QY	1981	GGCTCAAAGACCTTTCGGGCCAAAGGGCCCAATCAACCAATGTATACCAATGTGGAC	2040	Db	3061	GGCGATTTTCGACTCAGTGATCGACTCAATACATGTGTGTCACCCAGACAGTTCGAGC	3120
Db	1981	GGCTCAAAGACCTTTCGGGCCAAAGGGCCCAATCAACCAATGTATACCAATGTGGAC	2040	QY	3121	CTGGACCCGACCTTTCACCATTTGAGAGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3180
QY	2041	CAGGACTCTCGGTGGCAAGCGCCCGCGGGCGGTTCTTTGACACCATGCACTGTC	2100	Db	3121	CTGGACCCGACCTTTCACCATTTGAGAGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3180
Db	2041	CAGGACTCTCGGTGGCAAGCGCCCGCGGGCGGTTCTTTGACACCATGCACTGTC	2100	QY	3181	CAGCGGAGGACAGGACTGGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
QY	2101	GGCAGCTCGGACCTTTACTTGGTCAACAGGATGCGGATGTCATTCGCGTCCCGCGG	2160	Db	3181	CAGCGGAGGACAGGACTGGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
Db	2101	GGCAGCTCGGACCTTTACTTGGTCAACAGGATGCGGATGTCATTCGCGTCCCGCGG	2160	QY	3241	GAACGGCCCTCGGGCATGTTCGATTTCTCGGTCTGTGCGAGTGTATGACGGGGCTGT	3300
QY	2161	GGCGACAGGAGGAGCTTACTCTCCCCAGGCGCGTCTCTACTTTGAAGGGCTCTTCG	2220	Db	3241	GAACGGCCCTCGGGCATGTTCGATTTCTCGGTCTGTGCGAGTGTATGACGGGGCTGT	3300
Db	2161	GGCGACAGGAGGAGCTTACTCTCCCCAGGCGCGTCTCTACTTTGAAGGGCTCTTCG	2220	QY	3301	GCTTGTAGAGCTACGCGCCCGGAGACCTCAGTTAGGTTGCGGGCTTACCTTAAACACA	3360
QY	2221	GGCGGTCACCTGCTCTGCGGCTCGGGGACGCTGTGGGCACTTTTGGGCTGCGGTGTC	2280	Db	3301	GCTTGTAGAGCTACGCGCCCGGAGACCTCAGTTAGGTTGCGGGCTTACCTTAAACACA	3360
Db	2221	GGCGGTCACCTGCTCTGCGGCTCGGGGACGCTGTGGGCACTTTTGGGCTGCGGTGTC	2280	QY	3361	CAGGGTTGCCGTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCGCTCTTTACAGGCTC	3420
QY	2281	ACCCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCGGTGAGTCTATGGAAACCATATG	2340	Db	3361	CAGGGTTGCCGTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCGCTCTTTACAGGCTC	3420
Db	2281	ACCCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCGGTGAGTCTATGGAAACCATATG	2340	QY	3421	ACCCATAGAGCCCATTTCTGTCACGACTAAGCAGCAGGAGACAACTTCCCTAC	3480
QY	2341	CGGTCCCAGGCTTTCACGGCAAACTCGTCCCTCCGGCCGTACCGCAGACATTCACAGGTG	2400				

Db 3421 ACCACATAGACGCCCATTTCTTCTCCAGACTAAGCAGGAGGAGACAACTTCCCTAC 3480
Qy
3481 CTGGTAGCATACAGGCTACGGTGTGCGCGAGGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Db 3481 CTGGTAGCATACAGGCTACGGTGTGCGCGAGGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Qy 3541 CAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGCAGCGGCCCAAGCCCTCGTGTG 3600
Db 3541 CAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGCAGCGGCCCAAGCCCTCGTGTG 3600
Qy 3601 TATAGGCTGGAGCGCTTCAAAACAGAGTTTACTACACACACACCCCATAAACCAATACATC 3660
Db 3601 TATAGGCTGGAGCGCTTCAAAACAGAGTTTACTACACACACACCCCATAAACCAATACATC 3660
Qy 3661 ATGGCATGCATCGGCTGACCTGGAGTGTGCTGACAGCAGCGTGTGCTGAGCGGAG 3720
Db 3661 ATGGCATGCATCGGCTGACCTGGAGTGTGCTGACAGCAGCGTGTGCTGAGCGGAG 3720
Qy 3721 GTCTAGCAGCTCTGGCCCGGTATTGCCCTGACAAAGCAGCGTGTGCTGAGCGGAG 3780
Db 3721 GTCTAGCAGCTCTGGCCCGGTATTGCCCTGACAAAGCAGCGTGTGCTGAGCGGAG 3780
Qy 3781 ATCATCTTCTCGGAGGCGGCGCATCATTTCCCGACAGAGAAAGTCTTTTACCGGAGTTTC 3840
Db 3781 ATCATCTTCTCGGAGGCGGCGCATCATTTCCCGACAGAGAAAGTCTTTTACCGGAGTTTC 3840
Qy 3841 GATGAGATGGAAGTGGCGCTCACACCTCTTATCATCGACAGGAAATGACGCTCGCC 3900
Db 3841 GATGAGATGGAAGTGGCGCTCACACCTCTTATCATCGACAGGAAATGACGCTCGCC 3900
Qy 3901 GAACAATTCACAGAGGCAATCGGCTTCTCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
Db 3901 GAACAATTCACAGAGGCAATCGGCTTCTCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
Qy 3961 GCTGCTCCGCTGTGGAAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG 4020
Db 3961 GCTGCTCCGCTGTGGAAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG 4020
Qy 4021 TGGAAATTCATAGCGGAGTACAAATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCC 4080
Db 4021 TGGAAATTCATAGCGGAGTACAAATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCC 4080
Qy 4081 GCGATAGCATCACTGATGGCAATTCACAGCCTTATACAGCCTGCTCAGCAGCCGCTC 4140
Db 4081 GCGATAGCATCACTGATGGCAATTCACAGCCTTATACAGCCTGCTCAGCAGCCGCTC 4140
Qy 4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGTGGCGGCCAACTTGTCTCTCCAGCGCT 4200
Db 4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGTGGCGGCCAACTTGTCTCTCCAGCGCT 4200
Qy 4201 GCTTCTGCTTGTAGCGCGGATCGCTGGAGCGCTGTGGCAGCATAGGCTTGGG 4260
Db 4201 GCTTCTGCTTGTAGCGCGGATCGCTGGAGCGCTGTGGCAGCATAGGCTTGGG 4260
Qy 4261 AAGGTGCTTGGATATTTTGGCAGGTTATGGCAGGCTGGCAGCGGCTCGTGCC 4320
Db 4261 AAGGTGCTTGGATATTTTGGCAGGTTATGGCAGGCTGGCAGCGGCTCGTGCC 4320
Qy 4321 TTTAAGGTTCATAGCGCGAGATGCCCTTCCACCGAGGACCTGGTTAACCTACTCCCTGCT 4380
Db 4321 TTTAAGGTTCATAGCGCGAGATGCCCTTCCACCGAGGACCTGGTTAACCTACTCCCTGCT 4380
Qy 4381 ATCTCTCTCCCTGGCGGCTTGTGCTGGGCTGTGGCAGCATAGCTCGGCGAC 4440
Db 4381 ATCTCTCTCCCTGGCGGCTTGTGCTGGGCTGTGGCAGCATAGCTCGGCGAC 4440
Qy 4441 GTGGGCCAGGAGGAGGAGGCTGTGCAAGTGAACCGGCTGTAGCGTTCCGCTTCGCG 4500
Db 4441 GTGGGCCAGGAGGAGGAGGCTGTGCAAGTGAACCGGCTGTAGCGTTCCGCTTCGCG 4500
Qy 4501 GGTAAACCAAGTCTCCCGACGACATATGTGCTGAGAGCGAGCTGACGACGCTGCTACT 4560
Db 4501 GGTAAACCAAGTCTCCCGACGACATATGTGCTGAGAGCGAGCTGACGACGCTGCTACT 4560

Qy 4561 CAGATCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGGCTTACCAGTGGATCAAC 4620
Db 4561 CAGATCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGGCTTACCAGTGGATCAAC 4620
Qy 4621 GAGGACTCTCCACGCCATGCTCCGGCTGTGGCTTAAGAGATGTTTGGATTGGATATGC 4680
Db 4621 GAGGACTCTCCACGCCATGCTCCGGCTGTGGCTTAAGAGATGTTTGGATTGGATATGC 4680
Qy 4681 ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGCCCGATTTGCCGGA 4740
Db 4681 ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGCCCGATTTGCCGGA 4740
Qy 4741 GTCCCTCTTCTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGCGAGCGCATCATG 4800
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Qy 4801 CAAACCACTGCGCATGTGGAGCAGATCACCGGACATGTGAAGAGTTTCCATGAGG 4860
Db 4801 CAAACCACTGCGCATGTGGAGCAGATCACCGGACATGTGAAGAGTTTCCATGAGG 4860
Qy 4861 ATCTGGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTTCCCAATTAACGCGTAC 4920
Db 4861 ATCTGGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTTCCCAATTAACGCGTAC 4920
Qy 4921 ACCACGGGCTTGCACGCTTCCCGCGGCCAAATTTATCTAGGCGCTGTGGCGGGTG 4980
Db 4921 ACCACGGGCTTGCACGCTTCCCGCGGCCAAATTTATCTAGGCGCTGTGGCGGGTG 4980
Qy 4981 GCTGCTGAGAGTACGTGGAGCTTACGGGGTGGGGATTTCCACTGCTGACGGGCATG 5040
Db 4981 GCTGCTGAGAGTACGTGGAGCTTACGGGGTGGGGATTTCCACTGCTGACGGGCATG 5040
Qy 5041 ACCACTGACAAAGTAAAGTGCCTGTCAAGTTCCCGCCCCCGAAATTTCTTCAAGAAGTG 5100
Db 5041 ACCACTGACAAAGTAAAGTGCCTGTCAAGTTCCCGCCCCCGAAATTTCTTCAAGAAGTG 5100
Qy 5101 GATGGGTGGGTGTCACAGGTACGCTCCAGGTGCAACCCCTCTACGGGAGGAGTTC 5160
Db 5101 GATGGGTGGGTGTCACAGGTACGCTCCAGGTGCAACCCCTCTACGGGAGGAGTTC 5160
Qy 5161 ACATTCCTGGTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATCCGAGCCCGAA 5220
Db 5161 ACATTCCTGGTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATCCGAGCCCGAA 5220
Qy 5221 CCGGAGTAGCAGTGTCTCACTTCCATGCTCAGCGACCCCTCCACATTAACGGCGGAGAG 5280
Db 5221 CCGGAGTAGCAGTGTCTCACTTCCATGCTCAGCGACCCCTCCACATTAACGGCGGAGAG 5280
Qy 5281 GCTAAGCGTAGGCTGGCGAGGGATCTCCCTCTTGGCCAGCTCATCAGCTAGCCAG 5340
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Qy 5341 CTGCTGGCGCTTCTTGAAGGCAACATGCACTACCCGTATGACTCCCGGAGCGCTGAC 5400
Db 5341 CTGCTGGCGCTTCTTGAAGGCAACATGCACTACCCGTATGACTCCCGGAGCGCTGAC 5400
Qy 5401 CTCAATCAGAGCCCAACCTCTCTGTGGCGGAGAGTGGCGGAGAACATCAACCGCGTGGAG 5460
Db 5401 CTCAATCAGAGCCCAACCTCTCTGTGGCGGAGAGTGGCGGAGAACATCAACCGCGTGGAG 5460
Qy 5461 TCAGAAAATTAAGGTAGTAAATTTTGGACTCTTTTGGAGCGCTTCCAGCGGAGGAGTGA 5520
Db 5461 TCAGAAAATTAAGGTAGTAAATTTTGGACTCTTTTGGAGCGCTTCCAGCGGAGGAGTGA 5520
Qy 5521 AGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTCACAGAAATTTCCCTCGAGCGATG 5580
Db 5521 AGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTCACAGAAATTTCCCTCGAGCGATG 5580
Qy 5581 CCCATATGGGACGCCCGGATTAACAACCTCCTCACTGTTAGAGTCTCTGGAAGGACCCGAC 5640
Db 5581 CCCATATGGGACGCCCGGATTAACAACCTCCTCACTGTTAGAGTCTCTGGAAGGACCCGAC 5640

QY	1609	GAAGAGTCAAAATGGCTCTCTCAAGCGCTATTCAACAAAGGGGCTGAAGGATGCCAGAAG	1668
Db	1621	GAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGAAGGATGCCAGAAG	1680
QY	1669	GTACCCCATTTGATGGGAATCTGAATCTGGGGCCTCGTGSCACATGCTTTTACATGTGTTTAG	1728
Db	1681	GTACCCCATTTGATGGGAATCTGAATCTGGGGCCTCGTGSCACATGCTTTTACATGTGTTTAG	1740
QY	1729	TCGAGGTTAAAAAAGCTCTAGGCCCCCGGAACCAAGGGGAGCTGGTTTTCTTTGAAAAA	1788
Db	1741	TCGAGGTTAAAAAAGCTCTAGGCCCCCGGAACCAAGGGGAGCTGGTTTTCTTTGAAAAA	1800
QY	1789	CACGATAATACATGGCGCCTATTACGGCCTACTCCAAACAGACGCGAGAGCCTACTTGGC	1848
Db	1801	CACGATAATACATGGCGCCTATTACGGCCTACTCCAAACAGACGCGAGAGCCTACTTGGC	1860
QY	1849	TGCATCATCATAGCCTCACAGGCGCGGACAGGAACCAAGGTCGAGGGGGAGGTCCAGGTG	1908
Db	1861	TGCATCATCATAGCCTCACAGGCGCGGACAGGAACCAAGGTCGAGGGGGAGGTCCAGGTG	1920
QY	1909	GTCTCCACCGCAACACAAATCTTTCTGGCGACTGCGCTCAATGGCGTGTTGGACTGTCT	1968
Db	1921	GTCTCCACCGCAACACAAATCTTTCTGGCGACTGCGCTCAATGGCGTGTTGGACTGTCT	1980
QY	1969	TATCATGTGCGCGCTCAAGACCTTTGCGGCGCCAAAGGGGCCCAATCAACCCAAATGTAC	2028
Db	1981	TATCATGTGCGCGCTCAAGACCTTTGCGGCGCCAAAGGGGCCCAATCAACCCAAATGTAC	2040
QY	2029	ACCAATGTGGACAGGACCTGTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCTCTTGACA	2088
Db	2041	ACCAATGTGGACAGGACCTGTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCTCTTGACA	2100
QY	2089	CCATGCACTTGCSCAGCTCGGACCTTTACTTGGTCACGAGGACATGCCGATGTCATTCG	2148
Db	2101	CCATGCACTTGCSCAGCTCGGACCTTTACTTGGTCACGAGGACATGCCGATGTCATTCG	2160
QY	2149	GTGCGCGGGGGGCGCACAGCAGGGGAGGCTACTCTCCCGCAGGCGCGTCTCTACTTGG	2208
Db	2161	GTGCGCGGGGGGCGCACAGCAGGGGAGGCTACTCTCCCGCAGGCGCGTCTCTACTTGG	2220
QY	2209	AAGGGCTTTGGGCGGFTCACTGCTGTGCCCTCGGGGCACGCTGTGGGCGATCTTTCCG	2268
Db	2221	AAGGGCTTTGGGCGGFTCACTGCTGTGCCCTCGGGGCACGCTGTGGGCGATCTTTCCG	2280
QY	2269	GCTCCGCTGTGCACCCGAGGGGTGGGAAGCGGTGACTTTGTGTACCCGTGAGTCTATG	2328
Db	2281	GCTCCGCTGTGCACCCGAGGGGTGGGAAGCGGTGACTTTGTGTACCCGTGAGTCTATG	2340
QY	2329	GAACAACCTATGCGGTCCCCTGCTTCAAGCAACTCGTCCCTCCGCGCGTACCGAG	2388
Db	2341	GAACAACCTATGCGGTCCCCTGCTTCAAGCAACTCGTCCCTCCGCGCGTACCGAG	2400
QY	2389	ACATTCAGGTGGCCCATCTACAGGCCCTACTGTGTAGCGGCAAGAGCACTAAGTGGCG	2448
Db	2401	ACATTCAGGTGGCCCATCTACAGGCCCTACTGTGTAGCGGCAAGAGCACTAAGTGGCG	2460
QY	2449	GCTCGGTATGCACGCCAAGGATATAGGTCTGTGCTCTGAAACCGCTCGTCCGCCGAC	2508
Db	2461	GCTCGGTATGCACGCCAAGGATATAGGTCTGTGCTCTGAAACCGCTCGTCCGCCGAC	2520
QY	2509	CTAGGTTTCGGGCGTATATGTCTAAGGCACATGGTATCGACCTTAAACATCAGAACCGG	2568
Db	2521	CTAGGTTTCGGGCGTATATGTCTAAGGCACATGGTATCGACCTTAAACATCAGAACCGG	2580
QY	2569	GTAAAGACCATCACAGGGTGGCCCCCATCAAGTACTCCACTATGGCAAGTTTCTTCC	2628
Db	2581	GTAAAGACCATCACAGGGTGGCCCCCATCAAGTACTCCACTATGGCAAGTTTCTTCC	2640
QY	2629	GACGTTGTTGCTCTCGGGGCGCTATGACATCATTAATGTATGTAGTGCACCTCAACT	2688
Db	2641	GACGTTGTTGCTCTCGGGGCGCTATGACATCATTAATGTATGTAGTGCACCTCAACT	2700

QY	2689	GACTCGAACCATATCTCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGGCTCGGAGCG	2748
DB	2701	GACTCGAACCATATCTCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGGCTCGGAGCG	2760
QY	2749	CGACHTCGTCTGTCTCGCCACCGCTACGCCTCCGGGATCGGTCAACGTGCGACATCTCCAAC	2808
DB	2761	CGACHTCGTCTGTCTCGCCACCGCTACGCCTCCGGGATCGGTCAACGTGCGACATCTCCAAC	2820
QY	2809	ATCGAGGAGTGGTCTCTCGACACATGGAGAAATCCCTTTTATGCAAGGCCATCCCC	2868
DB	2821	ATCGAGGAGTGGTCTCTCGACACATGGAGAAATCCCTTTTATGCAAGGCCATCCCC	2880
QY	2869	ATCGAGACATCAAGGGGGGAGGCACTCATTTTCTGCCATTCCAAGAAGAAATGTGAT	2928
DB	2881	ATCGAGACATCAAGGGGGGAGGCACTCATTTTCTGCCATTCCAAGAAGAAATGTGAT	2940
QY	2929	GAGCTCGCGGAGCTGTCTCGGCTCGGACTCAATCTGTAGCATATATACCGGGGCTT	2988
DB	2941	GAGCTCGCGGAGCTGTCTCGGCTCGGACTCAATCTGTAGCATATATACCGGGGCTT	3000
QY	2989	GATGTATCCGTATACCAACTAGCGGAGACGTCAATTCTGTAGCAACGGACGCTCTAATG	3048
DB	3001	GATGTATCCGTATACCAACTAGCGGAGACGTCAATTCTGTAGCAACGGACGCTCTAATG	3060
QY	3049	ACGGGCTTTACGGCGATTTTCGACTCAGTGATCGACTGCAATATCATGTGTCAACCCAGACA	3108
DB	3061	ACGGGCTTTACGGCGATTTTCGACTCAGTGATCGACTGCAATATCATGTGTCAACCCAGACA	3120
QY	3109	GTCGACTTCAGCCGTGACCGGACCGCTTACCACTTCGAGACGACGACCGTCCCAAGACGGG	3168
DB	3121	GTCGACTTCAGCCGTGACCGGACCGCTTACCACTTCGAGACGACGACCGTCCCAAGACGGG	3180
QY	3169	GTGTCACGCTCGCACGGCGGAGGACGACTGTGTAGGGGACGAGTGGCATTTTACAGGTTT	3228
DB	3181	GTGTCACGCTCGCACGGCGGAGGACGACTGTGTAGGGGACGAGTGGCATTTTACAGGTTT	3240
QY	3229	GTGACTCCAGAGAAACGGCCCTCGGCATGTTTCGATTCTCTCGTTCGTGCGAGTGCTAT	3288
DB	3241	GTGACTCCAGAGAAACGGCCCTCGGCATGTTTCGATTCTCTCGTTCGTGCGAGTGCTAT	3300
QY	3289	GACCGGGCTGTGCTGGTATCAGACTCAGCCCGCCGAGACCTCAGTTAGTTTGGCGGT	3348
DB	3301	GACCGGGCTGTGCTGGTATCAGACTCAGCCCGCCGAGACCTCAGTTAGTTTGGCGGT	3360
QY	3349	TACCTAAACACACAGGTTGCCCGTCTGCCAGGACCATCTGGAGTTCTGGAGAGCGTTC	3408
DB	3361	TACCTAAACACACAGGTTGCCCGTCTGCCAGGACCATCTGGAGTTCTGGAGAGCGTTC	3420
QY	3409	TTTACAGGCTCACCACATAGACGCCATTTCTTGTCAGACTAAGCAGGACGAGAC	3468
DB	3421	TTTACAGGCTCACCACATAGACGCCATTTCTTGTCAGACTAAGCAGGACGAGAC	3480
QY	3469	AACTTCCCTTACCTGTGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCACCT	3528
DB	3481	AACTTCCCTTACCTGTGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCACCT	3540
QY	3529	CCATCTGGGACCAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGACGCGGCA	3588
DB	3541	CCATCTGGGACCAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGACGCGGCA	3600
QY	3589	ACGCCCCCTGTATAGGCTGGGACCGGTTCAAAACGAGGTTTACTACCAACACCCCCATA	3648
DB	3601	ACGCCCCCTGTATAGGCTGGGACCGGTTCAAAACGAGGTTTACTACCAACACCCCCATA	3660
QY	3649	ACCAATACATCATGSCATGCTGTGCGTGTGACCTGTGAGGTCGTACAGGACCTGGGTG	3708
DB	3661	ACCAATACATCATGSCATGCTGTGCGTGTGACCTGTGAGGTCGTACAGGACCTGGGTG	3720
QY	3709	CTGGTAGGCGGAGTCTTAGCAGCTCTGGCCGGTATTCCTTGACAAACAGGACGCTGTGTC	3768
DB	3721	CTGGTAGGCGGAGTCTTAGCAGCTCTGGCCGGTATTCCTTGACAAACAGGACGCTGTGTC	3780
QY	3769	ATTGTGGGACGATCATTTGTTCGGAAAGCGCGCCATCATTTCCCGACAGGGAAGTCTT	3828

3781	ATTGTGGCGAGGATCATCTTGTCCGNAAGCCGGCCATCATTCCTCCGACAGGGAAGTCTCT	3840	DB
3829	TACCGGAGTTTCGATGAGATGGAAGAGTGGCGCTTCACACTCCTCTTACATCATGAAAGGGA	3888	QY
3841	TACCGGAGTTTCGATGAGATGGAAGAGTGGCGCTTCACACTCCTCTTACATCATGAAAGGGA	3900	DB
3889	ATGCAGCTCCGCGAACAATTCMAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAG	3948	QY
3901	ATGCAGCTCCGCGAACAATTCMAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAG	3960	DB
3949	CAAGCGAGGCTGCTGCTCCCGTGGTGGAAATCCAAGTGGCGGACCTTCGAAGCCTTCTGG	4008	QY
3961	CAAGCGAGGCTGCTGCTCCCGTGGTGGAAATCCAAGTGGCGGACCTTCGAAGCCTTCTGG	4020	DB
4009	GCGAAGCATATGTGGAATTTCAATCAGCGGGAACAATATTTAGCAGGCTTGTCCACTCTG	4068	QY
4021	GCGAAGCATATGTGGAATTTCAATCAGCGGGAACAATATTTAGCAGGCTTGTCCACTCTG	4080	DB
4069	CCTGGCAACCCGCGATAGCATCTGATGCAATTCACAGCCTTATCACCAGCCGCTC	4128	QY
4081	CCTGGCAACCCGCGATAGCATCTGATGCAATTCACAGCCTTATCACCAGCCGCTC	4140	DB
4129	ACCACCCAAATACCTCTCTGTTTAAATCATCTGGGGGGATGGGTGGCCGCCAACTTGCT	4188	QY
4141	ACCACCCAAATACCTCTCTGTTTAAATCATCTGGGGGGATGGGTGGCCGCCAACTTGCT	4200	DB
4189	CCTCCACGCTGCTTCTGCTTTTCGTAGCGCCCGGCATCGTGGAGCGGCTTGTGGCAGC	4248	QY
4201	CCTCCACGCTGCTTCTGCTTTTCGTAGCGCCCGGCATCGTGGAGCGGCTTGTGGCAGC	4260	DB
4249	ATAGGCTTGGGAAGTCTGTTGTGATATTTTGGCAGGTTATGAGCAGGGTGGCAGGC	4308	QY
4261	ATAGGCTTGGGAAGTCTGTTGTGATATTTTGGCAGGTTATGAGCAGGGTGGCAGGC	4320	DB
4309	GCGCTGCTGGCTTTAAAGTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGCTAAC	4368	QY
4321	GCGCTGCTGGCTTTAAAGTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAAC	4380	DB
4369	CTACTCCCTGCTATCCTCTCCCTGGCGCCTAGTGTGCTGGGGTGTGTCGCGACGATA	4428	QY
4381	CTACTCCCTGCTATCCTCTCCCTGGCGCCTAGTGTGCTGGGGTGTGTCGCGACGATA	4440	DB
4429	CTGCGTGGCACTGTGGGCCAGGGAGGGGGTGTGCACTGATGATGAACCCGGCTGATAGCG	4488	QY
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4489	TTTCGCTTCGCGGGTAAACCACTCTCCGCCAGCACTATGTCCTGAGAGCAGCCTGCA	4548	QY
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4549	GCAGGTGCTCAGATTCCTCTGATGTTACCATCATCTCAGCTGCTGAAGAGCTTCAC	4608	QY
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4609	CAGTGGATCAACGAGGACTGCTCCAGCCATGCTCCGGCTCGTGCTTAAGAGATGTTTGG	4668	QY
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4669	GATTGGATATGACCGGTGTTGACTGATTTCAAGACCTTGCTCAGTCCAAAGCTCTGCGG	4728	QY
4681	GATTGGATATGACCGGTGTTGACTGATTTCAAGACCTTGCTCAGTCCAAAGCTCTGCGG	4740	DB
4729	CGATTCCGGGAGTCCCTCTCTCTCATGTCAAGTGGTACAAGGAGTCTGGCGGGGC	4788	QY
4741	CGATTCCGGGAGTCCCTCTCTCTCATGTCAAGTGGTACAAGGAGTCTGGCGGGGC	4800	DB
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4849	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACGTTGGCATGGAAATTCCTCC	4908	QY
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5029	GTGACGGCATGACCACTGACAAAGTAAAGTCCCGTGTGAGTTCCGGGCCCCGAAATTC	5088	QY
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568			

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Db	6001	TCCTACATGGA	CAGCGCCCTG	ATCA	CGCCAT	TGCGT	CGGAGGAAA	CCAA	GCTCCCC	6060
Qy	6049	ATCAATGCACT	GAGCAACTCT	TTTCT	CGCT	CAGCA	CAACAT	TGGT	TCTATGCT	6108
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Qy	6109	CGCAGCGCA	AGCCTCG	CGC	GAGA	AGGT	CACCTTT	GAC	GACATG	6168
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Qy	6229	CTATCCGTG	GAGGAGCGCT	GT	AA	GCTG	CAG	CGCCCC	CAATTC	6288
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Db	6661	TGTTTTG	ACTCA	AC	GGT	C	ACTG	AG	ATG	6720
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Db	6721	TGTGACTT	G	GGCCCC	CG	AAAG	CG	CA	CGG	6780
Qy	6769	GGGGCCCC	CTG	ACTA	ATTT	CT	AAAG	GG	CGAA	6828
Db	6781	GGGGCCCC	CTG	ACTA	ATTT	CT	AAAG	GG	CGAA	6840
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Qy	6949	ATCTGT	G	AAAG	CG	CGG	G	AT	CC	7008
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Qy	7009	ATGACT	G	AT	ACT	TG	CCCC	CT	G	7068
Db	7021	ATGACT	G	AT	ACT	TG	CCCC	CT	G	7080

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QY	7249	ATGATCCTGATGACTCATTTCTTCTCCATCTTTCTAGCTCAGGAACAACCTTGAAAAGCC	7308
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DEFINITION	Sequence 3 from Patent EP1043399.	linear	PAT 16-NOV-2000
ACCESSION	AX036254		
VERSION	AX036254.1	GI:11225870	
KEYWORDS			
SOURCE			Hepatitis C virus

RESULT 6
AX036254
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM Hepatitis C virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
 AUTHORS Bartenschlager, R.D.
 TITLE Hepatitis C virus cell culture system
 JOURNAL Patent: EP 1043399-A 3 11-OCT-2000;
 BARTENSCHLAGER RALF DR (DE)

FEATURES
 Location/Qualifiers
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 /organism="Hepatitis C virus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:11103"

ORIGIN

Query Match 99.6%; Score 7960.6; DB 6; Length 8001;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 7985; Conservative 0; Mismatches 4; Indels 12; Gaps 1;

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 DB 1 GCCAGCCCCGATTCGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAATCTATG 60

QY 61 TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGCGAGCCTCCAGGAC 120
 DB 61 TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGCGAGCCTCCAGGAC 120

QY 121 CCCCCCTCCGGAGAGCCATAGTGGTCTGCGGAACCGGTAGTACACCGGAATTCGCAG 180
 DB 121 CCCCCCTCCGGAGAGCCATAGTGGTCTGCGGAACCGGTAGTACACCGGAATTCGCAG 180

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QY 241 GCGAGCTGTAGCCGAGTAGTGTGGTTCGGAAGGCTTGTGTACTGTGCTGATAGG 300
 DB 241 GCGAGCTGTAGCCGAGTAGTGTGGTTCGGAAGGCTTGTGTACTGTGCTGATAGG 300

QY 301 GTGCTTGCAGTGCCCGGAGAGTCTGTAGACCGTGCACATAGAGCAGATCTCTAAC 360
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 DB 1441 GTGAAGGAGCAGTTCCTCTGGAAGTCTTCTGAAGCAAAACACGCTGTAGCGACCT 1500

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REFERENCE	1	artificial sequences; vectors.	
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TITLE	Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line		
JOURNAL	Science 285 (5424), 110-113 (1999)		
MEDLINE	99322193		
PUBMED	10390360		
REFERENCE	2 (bases 1 to 8001)		
AUTHORS	Bartenschlager, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY		
FEATURES	Location/Qualifiers		


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QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGAAACCGGTGAGTACACCGGAATTGCCAG 180
QY 181 GACGACGGGTCTTCTTGGATCAACCGCTCAATGCTCGAGATTTGGGGGTGCCCC 240
DB 181 GACGACGGGTCTTCTTGGATCAACCGCTCAATGCTCGAGATTTGGGGGTGCCCC 240
QY 241 GCGAGCTGTAGCCGAGTAGTGTGGTTCGCGAAAGGCTTGTGGTACTGTGCTGATAGG 300
DB 241 GCGAGCTGTAGCCGAGTAGTGTGGTTCGCGAAAGGCTTGTGGTACTGTGCTGATAGG 300
QY 301 GTGCTTGGAGTGCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTGGAGTGCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
QY 361 CTCGAAGAAAAACCAAA-----GGCGCGCCATGATTGAAACAAGATGATGTC 408
DB 361 CTCGAAGAAAAACCAAAAGTAAACCAACGAGCGCGCCATGATTGAAACAAGATGATGTC 420
QY 409 ACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGATCGGGCAACACAGA 468
DB 421 ACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGATCGGGCAACACAGA 480
QY 469 CAATCGGCTGCTCTATGATCGCGCGTGTTCGCGCTGTGACGCGGGCGCGCGGCTCTTT 528
DB 469 CAATCGGCTGCTCTATGATCGCGCGTGTTCGCGCTGTGACGCGGGCGCGCGGCTCTTT 528
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Dt 481 CAATCGGCTGCTCTGATGCGCGGTGTTCCGGCTGTTCAGCGCAGGGGCGCGCGGTTCTTT 540
Qy
Qy 529 TTGTCAAGACCGACCTGTTCGGTGCCCTGAATGAATCTGCAAGGAGGAGCGAGCGGGCTAT 588
Dt 541 TTGTCAAGACCGACCTGTTCGGTGCCCTGAATGAATCTGCAAGGAGGAGCGAGCGGGCTAT 600
Qy 589 CGTGGCTGGCCACGACGGGGGTTCTTTCGCGCAGCTGTCTCGAGTGTCTCACTGAAGCGG 648
Dt 601 CGTGGCTGGCCACGACGGGGGTTCTTTCGCGCAGCTGTCTCGAGTGTCTCACTGAAGCGG 660
Qy 649 GAAGGAGCTGGCTGCTATTGGGGGAGTGGCGGGGCAAGATCTCTGTCACTCAACCTTG 708
Dt 661 GAAGGAGCTGGCTGCTATTGGGGGAGTGGCGGGGCAAGATCTCTGTCACTCAACCTTG 720
Qy 709 CTCCTGCGGAGAAAGTATCCATCATGCTGATGCAATGCGGGGCTGCATACGCTTGATC 768
Dt 721 CTCCTGCGGAGAAAGTATCCATCATGCTGATGCAATGCGGGGCTGCATACGCTTGATC 780
Qy 769 CGGCTACCTGCCATTCGACCAACCAAGCGAAACATCGCATCGAGGAGCAGTACTCGGA 828
Dt 781 CGGCTACCTGCCATTCGACCAACCAAGCGAAACATCGCATCGAGGAGCAGTACTCGGA 840
Qy 829 TGAAGCCGGTCTTGTCGATCAGGATGATCTGGAAGAGGATCAGGGGCTCGCGCCAG 888
Dt 841 TGAAGCCGGTCTTGTCGATCAGGATGATCTGGAAGAGGATCAGGGGCTCGCGCCAG 900
Qy 889 CCGAATGTTGCGCAGGCTCAAGCGCGGATGCGCGAGCGGAGGATCTCGTGTGACCC 948
Dt 901 CCGAATGTTGCGCAGGCTCAAGCGCGGATGCGCGAGCGGAGGATCTCGTGTGACCC 960
Qy 949 ATGCGGATGCTGCTTCCGCAATATCATGTTGAAATGCGCGCTTTCTGGATTCATCG 1008
Dt 961 ATGCGGATGCTGCTTCCGCAATATCATGTTGAAATGCGCGCTTTCTGGATTCATCG 1020
Qy 1009 ACTGTGCGCGGCTGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGTGATA 1068
Dt 1021 ACTGTGCGCGGCTGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGTGATA 1080
Qy 1069 TTGCTGAAGAGCTTGGCGGGGATGAGGCTGACCGCTTCCTGCTGCTTTACGATTCGCG 1128
Dt 1081 TTGCTGAAGAGCTTGGCGGGGATGAGGCTGACCGCTTCCTGCTGCTTTACGATTCGCG 1140
Qy 1129 CTCGGATTCGACGCGATCGCTTCTATCGCTTCTTGACGAGTCTCTCTGAGTTTAAA 1188
Dt 1141 CTCGGATTCGACGCGATCGCTTCTATCGCTTCTTGACGAGTCTCTCTGAGTTTAAA 1200
Qy 1189 CAGACCAACAGGTTCCCTCTAGCGGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT 1248
Dt 1201 CAGACCAACAGGTTCCCTCTAGCGGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT 1260
Qy 1249 AAGCTTACTGGCGAAGCCGCTTGGATTAAGCGCGGTGTGGTGTGCTATATGTTATTT 1308
Dt 1261 AAGCTTACTGGCGAAGCCGCTTGGATTAAGCGCGGTGTGGTGTGCTATATGTTATTT 1320
Qy 1309 TCCACCATATTCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTCTTG 1368
Dt 1321 TCCACCATATTCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTCTTG 1380
Qy 1369 ACAGCATTCCTAGGGTCTTTCCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGTC 1428
Dt 1381 ACAGCATTCCTAGGGTCTTTCCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGTC 1440
Qy 1429 GTGAAGGAAGAGTCTCTCTGGAAGCTTCTTGAAGACAAACAGTCTGTAGGACCCCTT 1488
Dt 1441 GTGAAGGAAGAGTCTCTCTGGAAGCTTCTTGAAGACAAACAGTCTGTAGGACCCCTT 1500
Qy 1489 TGCAAGCAGCGGAACCCCGACCTGGCGCAGAGTGCTCTGGCGCAAAAGCCACAGTGA 1548
Dt 1501 TGCAAGCAGCGGAACCCCGACCTGGCGCAGAGTGCTCTGGCGCAAAAGCCACAGTGA 1560
Qy 1549 TAAGATACACTGCAAGGGGCAACACCCCGAGTGCACGCTTGTGAGTGTGATGTTGTG 1608
Dt 1561 TAAGATACACTGCAAGGGGCAACACCCCGAGTGCACGCTTGTGAGTGTGATGTTGTG 1620

Qy 1609 GAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGGATGCCAGAAG 1668
Dt 1621 GAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGGATGCCAGAAG 1680
Qy 1669 GTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTATCATGTGTTAG 1728
Dt 1681 GTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTATCATGTGTTAG 1740
Qy 1729 TCGAGGTTAAAAAAGCTCTAGGCCCCCGGAAACAACGAGGAGCGTGGTCTTCTTTGAAAAA 1788
Dt 1741 TCGAGGTTAAAAAAGCTCTAGGCCCCCGGAAACAACGAGGAGCGTGGTCTTCTTTGAAAAA 1800
Qy 1789 CAGGATAATACCAATGGCGCTATTACGGCTCTACTCCCAACAGACGCGAGGCTACTTTGGC 1848
Dt 1801 CAGGATAATACCAATGGCGCTATTACGGCTCTACTCCCAACAGACGCGAGGCTACTTTGGC 1860
Qy 1849 TGCATCATCTACTAGCCTCACAGGCGGAGCAGGAACAGGTCGAGGGGAGGTCCAGGTG 1908
Dt 1861 TGCATCATCTACTAGCCTCACAGGCGGAGCAGGAACAGGTCGAGGGGAGGTCCAGGTG 1920
Qy 1909 GTCTCCACCGCAACAAATCTTTCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTC 1968
Dt 1921 GTCTCCACCGCAACAAATCTTTCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTC 1980
Qy 1969 TATCATGGTGCCTGGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCAACCAATGTAC 2028
Dt 1981 TATCATGGTGCCTGGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCAACCAATGTAC 2040
Qy 2029 ACCAATGTGACACAGACCTCGCTCGGTGCAAGCGCCCCCGGGCGCTTCTCTTGACA 2088
Dt 2041 ACCAATGTGACACAGACCTCGCTCGGTGCAAGCGCCCCCGGGCGCGTCTCTTGACA 2100
Qy 2089 CCATGCACTGCGCGCAGCTCGGACCTTTACTTGGTCAACGAGGATGCGGATGCAATTCG 2148
Dt 2101 CCATGCACTGCGCGCAGCTCGGACCTTTACTTGGTCAACGAGGATGCGGATGCAATTCG 2160
Qy 2149 GTGCGCGGGGGGCGACAGCAGGGGAGCTACTCTCCCGCAGGCCGCTCTCTACTTG 2208
Dt 2161 GTGCGCGGGGGGCGACAGCAGGGGAGCTACTCTCTCCCGCAGGCCGCTCTCTACTTG 2220
Qy 2209 AAGGGCTCTTCGGCGGTCCACTGCTGCGCCCTCGGGGCAACGCTGTGGGCATCTTTTCG 2268
Dt 2221 AAGGGCTCTTCGGCGGTCCACTGCTGCGCCCTCGGGGCAACGCTGTGGGCATCTTTTCG 2280
Qy 2269 GCTGCGGTGTCACCCGAGGGTTCGGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATG 2328
Dt 2281 GCTGCGGTGTCACCCGAGGGTTCGGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATG 2340
Qy 2329 GAAACCACTATGCGGTCCCGGTCTTTCAGCGGCAACTCTGTCCTCCCTCGGGCGGTACCGCAG 2388
Dt 2341 GAAACCACTATGCGGTCCCGGTCTTTCAGCGGCAACTCTGTCCTCCCTCGGGCGGTACCGCAG 2400
Qy 2389 ACATTCAGGTGCGCCATCTACACGCGCTTACTGCTAGCGGCAAGACACTAAGGTGCGC 2448
Dt 2401 ACATTCAGGTGCGCCATCTACACGCGCTTACTGCTAGCGGCAAGACACTAAGGTGCGC 2460
Qy 2449 GCTGCGGTATGACCCCAAGGGTATAAGGTGCTTGTCTCTGAAACCCGTCGTCGCGCCACC 2508
Dt 2461 GCTGCGGTATGACCCCAAGGGTATAAGGTGCTTGTCTCTGAAACCCGTCGTCGCGCCACC 2520
Qy 2509 CTAGGTTTCGGGGGTATATGCTAAGGCACTGGTATCGACCTTAACCATCAGAACCGG 2568
Dt 2521 CTAGGTTTCGGGGGTATATGCTAAGGCACTGGTATCGACCTTAACCATCAGAACCGG 2580
Qy 2569 GTAAGGACCATCACCGGGTGCCTCATCAGCTACTCCACCTATGCAAGTTCCTTGGC 2628
Dt 2581 GTAAGGACCATCACCGGGTGCCTCATCAGCTACTCCACCTATGCAAGTTCCTTGGC 2640
Qy 2629 GACGGTGGTGTCTCTGGGGCGCTATGACATCATATATGATGATGAGTGCCTCAACT 2688
Dt 2641 GACGGTGGTGTCTCTGGGGCGCTATGACATCATATATGATGATGAGTGCCTCAACT 2700

Qy	2689	GACTCGACCACTATCTCTGGGCATCGGCACAGCTCCTGGACCAAGCGGAGACGGCTGGAGCG	27448
Db	2701	GACTCGACCACTATCTCTGGGCATCGGCACAGCTCCTGGACCAAGCGGAGACGGCTGGAGCG	2760
Qy	2749	CGACTCGTGTGCTCGCCACCGCTACGCCCTCGGGATCGGTCAACCGTGCACATCCAAC	2808
Db	2761	CGACTCGTGTGCTCGCCACCGCTACGCCCTCGGGATCGGTCAACCGTGCACATCCAAC	2820
Qy	2809	ATCGAGGAGTGGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGACCATCCCT	2868
Db	2821	ATCGAGGAGTGGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGACCATCCCT	2880
Qy	2869	ATCGAGACCACTCAAGGGGGGAGGCACCTCATTTTCTGGCCATTCCTCAGAGAAATGTAT	2928
Db	2881	ATCGAGACCACTCAAGGGGGGAGGCACCTCATTTTCTGGCCATTCCTCAGAGAAATGTAT	2940
Qy	2929	GAGCTCGCCCGAAGCTGTCCGGCCTCGGACTCAATGCTGTAGCATATTAACGGGGCCTT	2988
Db	2941	GAGCTCGCCCGAAGCTGTCCGGCCTCGGACTCAATGCTGTAGCATATTAACGGGGCCTT	3000
Qy	2989	GATGTATCCGTGCATACCAATAGCGGAGACGTCAATTGCTGTAGCAACGGACGCTCTAATG	3048
Db	3001	GATGTATCCGTGCATACCAATAGCGGAGACGTCAATTGCTGTAGCAACGGACGCTCTAATG	3060
Qy	3049	ACGGGCTTTTACCGGCGATTTTCGACTCAGTGATCGACTGCAATACATGTGCACCCAGACA	3108
Db	3061	ACGGGCTTTTACCGGCGATTTTCGACTCAGTGATCGACTGCAATACATGTGCACCCAGACA	3120
Qy	3109	GTGCACCTTCAGCCTCGGACCCGACCTTCAACATTGAGACGACGACCGTGCACAAAGACGG	3168
Db	3121	GTGCACCTTCAGCCTCGGACCCGACCTTCAACATTGAGACGACGACCGTGCACAAAGACGG	3180
Qy	3169	GTGTACGCTCGCACGGCGGAGGACGACCTGTAGGGGACAGTATGGGCAATTAACAGTTT	3228
Db	3181	GTGTACGCTCGCACGGCGGAGGACGACCTGTAGGGGACAGTATGGGCAATTAACAGTTT	3240
Qy	3229	GTGACTCCAGGAGAACGGCCCTCTGGGCATGTTTCAATTCCTCGTTCGTGCGAGTGCTAT	3288
Db	3241	GTGACTCCAGGAGAACGGCCCTCTGGGCATGTTTCAATTCCTCGTTCGTGCGAGTGCTAT	3300
Qy	3289	GACGGGGCTGTGCTTGGTACGAGCTCACGGCCGCGAGACCTCAGTTAGTTTCGGGCT	3348
Db	3301	GACGGGGCTGTGCTTGGTACGAGCTCACGGCCGCGAGACCTCAGTTAGTTTCGGGCT	3360
Qy	3349	TACCTAAACACACAGAGTTTCCCGTCTGCCAGGACCATCTGGAGTTCTCGGAGAGCGTC	3408
Db	3361	TACCTAAACACACAGAGTTTCCCGTCTGCCAGGACCATCTGGAGTTCTCGGAGAGCGTC	3420
Qy	3409	TTTACAGGCTCACCCACATAGACGCCATTTCTTGTCCAGACTAAGCAGGACGAGGAC	3468
Db	3421	TTTACAGGCTCACCCACATAGACGCCATTTCTTGTCCAGACTAAGCAGGACGAGGAC	3480
Qy	3469	AACCTTCCCTTACCTGTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGGTCCACCT	3528
Db	3481	AACCTTCCCTTACCTGTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGGTCCACCT	3540
Qy	3529	CCATCGTGGACCAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCACGGGCCA	3588
Db	3541	CCATCGTGGACCAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCACGGGCCA	3600
Qy	3589	ACGCCCTGTGTATAGGCTGGGAGCCGTTCAAACGAGGTTACTACACACACCCCAT	3648
Db	3601	ACGCCCTGTGTATAGGCTGGGAGCCGTTCAAACGAGGTTACTACACACACCCCAT	3660
Qy	3649	ACCAAAATACATCATGGCATGCTCGGCTGCACCTGGAGTTCGTACAGACCTCGGGTG	3708
Db	3661	ACCAAAATACATCATGGCATGCTCGGCTGCACCTGGAGTTCGTACAGACCTCGGGTG	3720
Qy	3709	CTGGTAGCGGAGTCTTAGAGCTCTGGCCGCGTATTGGCTGCACACAGCAGCGTGGTC	3768
Db	3721	CTGGTAGCGGAGTCTTAGAGCTCTGGCCGCGTATTGGCTGCACACAGCAGCGTGGTC	3780
Qy	3769	ATTGTGGCAGGATCATCTTGTCCGGAAGGCGCGCCATCATTTCCGACAGGGAAGTCTT	3828

Db 4861 GGTTCATGAGGATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGCATGGAAATTCCTCCC 4920
Qy 4909 ATTAACGGGTACACACGGGCGCCCTGTCACGCCCTCTCCCGGGCGCAAAATTAATTTAGGGCG 4968
Db 4921 ATTAACGGGTACACACGGGCGCCCTGTCACGCCCTCTCCCGGGCGCAAAATTAATTTAGGGCG 4980
Qy 4969 CTGTGGGGGTGCTGCTGAGGAGTAGTGTCAGAGGTTACGGGGGTGGGGATTTCCACTAC 5028
Db 4981 CTGTGGGGGTGCTGCTGAGGAGTAGTGTCAGAGGTTACGGGGGTGGGGATTTCCACTAC 5040
Qy 5029 GTGACGGCATGACCACTGACAAAGTAAAGTGGCCGTGTGTCAGGTTCCGGGCCCGCAATTC 5088
Db 5041 GTGACGGCATGACCACTGACAAAGTAAAGTGGCCGTGTGTCAGGTTCCGGGCCCGCAATTC 5100
Qy 5089 TTCAAGAAGTGGGTGGGGTGGCAAGGTACGCTCAGCGGTGCAAAACCCCTCCCTA 5148
Db 5101 TTCAAGAAGTGGGTGGGGTGGCAAGGTACGCTCAGCGGTGCAAAACCCCTCCCTA 5160
Qy 5149 CGGGAGGAGTACATTTCTGTGTGGGCTCAATCAATACCTGTTGGGTGTCAGAGTCCCA 5208
Db 5161 CGGGAGGAGTACATTTCTGTGTGGGCTCAATCAATACCTGTTGGGTGTCAGAGTCCCA 5220
Qy 5209 TGGGAGCCGAAACGGGACGTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAATT 5268
Db 5221 TGGGAGCCGAAACGGGACGTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAATT 5280
Qy 5269 ACGGGGAGACGGCTAAGCGTAGGCTGGCGAGGGGATCTCCCTCTCTTGGGCCAGGTCA 5328
Db 5281 ACGGGGAGACGGCTAAGCGTAGGCTGGCGAGGGGATCTCCCTCTCTTGGGCCAGGTCA 5340
Qy 5329 TCAGCTAGCAGTGTCTGCGCTTCTTGAAGCAACATGCACTACCCGTCTGACTCC 5388
Db 5341 TCAGCTAGCAGTGTCTGCGCTTCTTGAAGCAACATGCACTACCCGTCTGACTCC 5400
Qy 5389 CCGGACGCTGACCTCATCGAGGCGCAACCTCTGTGGCGGAGAGATGGGCGGGAATC 5448
Db 5401 CCGGACGCTGACCTCATCGAGGCGCAACCTCTGTGGCGGAGAGATGGGCGGGAATC 5460
Qy 5449 ACCCGGTGAGTCAGAAAATAAGTAGTAATTTTGGACTCTTTCGAGCGCTTCCAAAGCG 5508
Db 5461 ACCCGGTGAGTCAGAAAATAAGTAGTAATTTTGGACTCTTTCGAGCGCTTCCAAAGCG 5520
Qy 5509 GAGGAGTACAGAGGAGATCCGTTCCGGCGAGATCTCGGAGGTCCAGGAATTC 5568
Db 5521 GAGGAGTACAGAGGAGATCCGTTCCGGCGAGATCTCGGAGGTCCAGGAATTC 5580
Qy 5569 CCTCGAGCATGCCATATGCGGACGCGCGGATTTACAAACCTCCACTGTGTAGAGTCTCG 5628
Db 5581 CCTCGAGCATGCCATATGCGGACGCGCGGATTTACAAACCTCCACTGTGTAGAGTCTCG 5640
Qy 5629 AAGGACCGGACTACGTCCTTCAGTGGTACACGGGTGTCATGTCGCGCTGCGCAAGGCC 5688
Db 5641 AAGGACCGGACTACGTCCTTCAGTGGTACACGGGTGTCATGTCGCGCTGCGCAAGGCC 5700
Qy 5689 CCTCCGATACACCTCCACGAGGAGAGAGCGGTGCTCTGTGTCAGAAATCTTACCGTCT 5748
Db 5701 CCTCCGATACACCTCCACGAGGAGAGAGCGGTGCTCTGTGTCAGAAATCTTACCGTCT 5760
Qy 5749 TCTGCTTGGCGAGCTCGCCACAAAGACCTTTCGGCAGCTCCGAATCGTGGCGCTCGAC 5808
Db 5761 TCTGCTTGGCGAGCTCGCCACAAAGACCTTTCGGCAGCTCCGAATCGTGGCGCTCGAC 5820
Qy 5809 AGCGGACGGGACGGGCTCTCTGACACGGCTTCCGACGAGCGGAGCGGAGTCCGAC 5868
Db 5821 AGCGGACGGGACGGGCTCTCTGACACGGCTTCCGACGAGCGGAGCGGAGTCCGAC 5880
Qy 5869 GTTGAGTGTACTCTCTCATGCCCTTGAAGGGGAGCGGGGATCCGATCTCAGC 5928
Db 5881 GTTGAGTGTACTCTCTCATGCCCTTGAAGGGGAGCGGGGATCCGATCTCAGC 5940
Qy 5929 GACGGGTCTTGGTCTACCGTAAGCGAGGAGGTAGTGAGGACGTCGTCGTGCTCGATG 5988
Db 5941 GACGGGTCTTGGTCTACCGTAAGCGAGGAGGTAGTGAGGACGTCGTCGTGCTCGATG 6000

Qy 5989 TCCTACACATGACAGCGCGCTGTATCAGCCATGCTGCTGGAGGAAACCAAGCTGCC 6048
Db 6001 TCCTACACATGACAGCGCGCTGTATCAGCCATGCTGCTGGAGGAAACCAAGCTGCC 6060
Qy 6049 ATCAATGCACTGAGCAACTCTTTGCTCCGTCAACACAACCTTGTCTATGCTACAACATCT 6108
Db 6061 ATCAATGCACTGAGCAACTCTTTGCTCCGTCAACACAACCTTGTCTATGCTACAACATCT 6120
Qy 6109 CGCAGCGCAAGCTCGCGCAGAAAGAGTCACTTTGACAGACTGCGAGTCTTGGAGCAC 6168
Db 6121 CGCAGCGCAAGCTCGCGCAGAAAGAGTCACTTTGACAGACTGCGAGTCTTGGAGCAC 6180
Qy 6169 CACTACCGGACGCTCTCAAGGAGTGAAGCGCAAGCGCTCCACAGTTAAGGCTAAACTT 6228
Db 6181 CACTACCGGACGCTCTCAAGGAGTGAAGCGCAAGCGCTCCACAGTTAAGGCTAAACTT 6240
Qy 6229 CTATCCGTGAGGAAGCTCTTAAGCTGACGCCGCCCACTTCGGGCCAGATCTAAATTTGGC 6288
Db 6241 CTATCCGTGAGGAAGCTCTTAAGCTGACGCCGCCCACTTCGGGCCAGATCTAAATTTGGC 6300
Qy 6289 TATGGGCAAAAGACGTCGCGGAACTTATCAGCAAGCGCGTTAACCAATCCCGTCCGTG 6348
Db 6301 TATGGGCAAAAGACGTCGCGGAACTTATCAGCAAGCGCGTTAACCAATCCCGTCCGTG 6360
Qy 6349 TGGAAAGACTTGTGGAAGACACTGAGACACCAATTTGACACCACTCATGCGCAAAAAT 6408
Db 6361 TGGAAAGACTTGTGGAAGACACTGAGACACCAATTTGACACCACTCATGCGCAAAAAT 6420
Qy 6409 GAGGTTTTCGCTCAACACAGAGAGGGGGCGCAAGCGAGCTCGCTTATGCTATTC 6468
Db 6421 GAGGTTTTCGCTCAACACAGAGAGGGGGCGCAAGCGAGCTCGCTTATGCTATTC 6480
Qy 6469 CCAGATTTGGGGTTCGTGTGTCGAGAAATGGCCCTTTACGATGTGCTTCCACCCTC 6528
Db 6481 CCAGATTTGGGGTTCGTGTGTCGAGAAATGGCCCTTTACGATGTGCTTCCACCCTC 6540
Qy 6529 CCTCAGCCCTGTAGGGCTCTTATACGAGTTCGATACCTCTCTGACAGCGGTGCGAG 6588
Db 6541 CCTCAGCCCTGTAGGGCTCTTATACGAGTTCGATACCTCTCTGACAGCGGTGCGAG 6600
Qy 6589 TTCTGTGTAATGCCTGGAAAGCGAAATGCCTATGCGCTTCGATATGACACCCGC 6648
Db 6601 TTCTGTGTAATGCCTGGAAAGCGAAATGCCTATGCGCTTCGATATGACACCCGC 6660
Qy 6649 TGTGTTGACTCAACGGTCACTGAGAAATGACATCCGTGTTGAGGAGTCAATCTTACCAATGT 6708
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Db 6721 TGTGACTGACGACAGCTCGGTAAATAACCTCAATGTTTAAAGGGCGCTTGGGCC 6780
Qy 6769 GGGGGCCCCCTGACTAATTTCTAAAGGCGAGAACTGGGGCTATCGCCGTGCGCGGAGC 6828
Db 6781 GGGGGCCCCCTGACTAATTTCTAAAGGCGAGAACTGGGGCTATCGCCGTGCGCGGAGC 6840
Qy 6829 GGTGTACTGACGACAGCTCGGTAAATAACCTCAATGTTTAAAGGGCGCTTGGGCC 6888
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Qy 6949 ATCTGTAAGGCGGGGACCCCAAGAGAGAGCGAGCGCTTACGGGCTTTCACGGAGGCT 7008
Db 6961 ATCTGTAAGGCGGGGACCCCAAGAGAGAGCGAGCGCTTACGGGCTTTCACGGAGGCT 7020
Qy 7009 ATGACTAGATACCTGTCGCCCTTGGGGACCCCGCCAAACCAAGATACGACTTGGAGTTG 7068
Db 7021 ATGACTAGATACCTGTCGCCCTTGGGGACCCCGCCAAACCAAGATACGACTTGGAGTTG 7080

Qy	7069	ATAACATCATGCTCTCCATATGTGTAGTCCGCGACGATGCACTTGCACAAAGGTTGAC	7129
Db	7081	ATAACATCATGCTCTCCATATGTGTAGTCCGCGCACCATGCACTGCGCAAAAGGTTGAC	7140
Qy	7129	TATCTCACCGTGACCCACACCCCTTTGCGGGCTCGGTGGGAGACAGCTAGACAC	7188
Db	7141	TATCTCACCGTGACCCACACCCCTTTGCGGGCTCGGTGGGAGACAGCTAGACAC	7200
Qy	7189	ACTCCAGTCAATTCTCGCTAGGCAACATCATATGTATGCGCCACCTTTGTGGGCAAGG	7248
Db	7201	ACTCCAGTCAATTCTCGCTAGGCAACATCATATGTATGCGCCACCTTTGTGGGCAAGG	7260
Qy	7249	ATGATTCCTGATGACTCATTTCTTCTCATCTCTTAGCTCAGGAACAACCTTGAAAAAGCC	7308
Db	7261	ATGATTCCTGATGACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACCTTGAAAAAGCC	7320
Qy	7309	CTAGATTGTCAGATCTACGGGGCTGTATCTCCANTGAGCCATTGACCTACCTCAGATC	7368
Db	7321	CTAGATTGTCAGATCTACGGGGCTGTATCTCCANTGAGCCATTGACCTACCTCAGATC	7380
Qy	7369	ATTCAAACGACTCCATGGCTTTAGCGCAATTTTCACTCCATATAGTTACTCTCCAGGTGAGATC	7428
Db	7381	ATTCAAACGACTCCATGGCTTTAGCGCAATTTTCACTCCATATAGTTACTCTCCAGGTGAGATC	7440
Qy	7429	AATAGGTGGCTTCATGCCCTCAGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACAT	7488
Db	7441	AATAGGTGGCTTCATGCCCTCAGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACAT	7500
Qy	7489	CGGGCCAGAGTGTCCGGCTTAGGCTACTGTCCTCAGGGGGGAGGGCTGCCACTTTGGCC	7548
Db	7501	CGGGCCAGAGTGTCCGGCTTAGGCTACTGTCCTCAGGGGGGAGGGCTGCCACTTTGGCC	7560
Qy	7549	AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCG	7608
Db	7561	AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCG	7620
Qy	7609	TCCAGTTGGATTATCCAGCTGGTTGCTGCTGGTTACGCGGGGGAGACATATATCAC	7668
Db	7621	TCCAGTTGGATTATCCAGCTGGTTGCTGCTGGTTACGCGGGGGAGACATATATCAC	7680
Qy	7669	AGCCTGTCTGTGCGCCGACCCCGTGGTTCAATGTGTGGCTACTCTCTACTTTTCTGTAGGG	7728
Db	7681	AGCCTGTCTGTGCGCCGACCCCGTGGTTCAATGTGTGGCTACTCTCTACTTTTCTGTAGGG	7740
Qy	7729	GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACACATCCAGGCCAATPAGG	7788
Db	7741	GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACACATCCAGGCCAATPAGG	7800
Qy	7789	CCATCTCTGTTTTTTTCCCTTT	7848
Db	7801	CCATCTCTGTTTTTTTCCCTTT	7860
Qy	7849	TTTTTCTCCTTTTTTTTTTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7908
Db	7861	TTTTTCTCCTTTTTTTTTTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7920
Qy	7909	CCTAGTCACGGCTAGCTGTCAAAGGTCGGTGAGCCGCTTGACCTGCACAGAGTGTCTGATC	7968
Db	7921	CCTAGTCACGGCTAGCTGTCAAAGGTCGGTGAGCCGCTTGACCTGCACAGAGTGTCTGATC	7980
Qy	7969	TGCGCTCTCTGCGAGATCAAGT	7989
Db	7981	TGCGCTCTCTGCGAGATCAAGT	8001

RESULT 8

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SOURCE

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linear PAT 18-DEC-2003

8001 bp
US 6630343

US 6630343.

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VERSION AX036259.1 GI:11225875
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SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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1 Bartschschlager,R.D.
AUTHORS Hepatitis c virus cell culture system
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[illegible]

RESULT 11

AX036257
LOCUS AX036257 8001 bp DNA linear PAT 16-NOV-2000
SEQUENCE 6 from Patent EP1043399.
ACCESSION AX036257
VERSION AX036257.1 GI:11225873
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE
1 Bartschslager.R.D.
AUTHORS
Hepatitis C virus cell culture system
TITLE Patent: EP 1043399-A 6 11-OCT-2000;
JOURNAL BARTENSCHLAGER RALF DR (DE)
FEATURES
Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;
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Db	1801	CACGATATAACATAGCGGCCCTATTACGCGCCTACTCCAAACAGACGCGAGGCGCTACTTTGGC	1860	Qy	2929	GAGCTCCGCGGGAAGCTGTCTCGGCTCGGACTCAATGCTAGCATATTACCGGGCCCTT	2988
Qy	1849	TGCATCATCTAGCCTCACAGGCGGGACAGGAACACAGGTCGAGGGGGAGGTCCAGGTG	1908	Db	2941	GAGCTCCGCGGGAAGCTGTCTCGGCTCGGACTCAATGCTAGCATATTACCGGGCCCTT	3000
Db	1861	TGCATCATCTAGCCTCACAGGCGGGACAGGAACACAGGTCGAGGGGGAGGTCCAAAGTG	1920	Qy	2989	GATGTATCCGTCTATACCAACTAGCGGAGAGCTGATTCGCTAGCAACGAGCGCTCTAATG	3048
Qy	1909	GTCTCCACCGGCAACACATCTTTCTTCTGGCGACCTCGCTCAATGCGGTGTGTGACTGTC	1968	Db	3001	GATGTATCCGTCTATACCAACTAGCGGAGAGCTGATTCGCTAGCAACGAGCGCTCTAATG	3060
Db	1921	GTCTCCACCGGCAACACATCTTTCTTCTGGCGACCTCGCTCAATGCGGTGTGTGACTGTC	1980	Qy	3049	ACGGGCTTTTACCGGCGAATTCGACTCAGTGATCACTGCAATACATATGTCACCCAGACA	3108
Qy	1969	TATCATGCTGCGGCTCAAGACCTTTGCGCGCCCAAGGCGCCCAATCACCACAAATGTAC	2028	Db	3061	ACGGGCTTTTACCGGCGAATTCGACTCAGTGATCACTGCAATACATATGTCACCCAGACA	3120
Db	1981	TATCATGCTGCGGCTCAAGACCTTTGCGCGCCCAAGGCGCCCAATCACCACAAATGTAC	2040	Qy	3109	GTGACTTCAGCTTGAGACCGGACCTTCACTGAGAGAGCGAGCGCTGCCACAAGACGCG	3168
Qy	2029	ACCAATGTGACACGAGCACTCGTGGGTGGCAAGCGGCCCCCGGGGCGGCTTCCTTGACA	2088	Db	3121	GTGACTTCAGCTTGAGACCGGACCTTCACTGAGAGAGCGAGCGCTGCCACAAGACGCG	3180
Db	2041	ACCAATGTGACACGAGCACTCGTGGGTGGCAAGCGGCCCCCGGGGCGGCTTCCTTGACA	2100	Qy	3169	GTGTCAGCTCGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3228
Qy	2089	CCATGCACTCTGGGAGCTCGGACCTTTACTTGTGTCAGGAGGATGCGGATGATTCCTCG	2148	Db	3181	GTGTCAGCTCGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3240
Db	2101	CCATGCACTCTGGGAGCTCGGAGCTTTACTTGTGTCAGGAGGATGCGGATGATTCCTCG	2160	Qy	3229	GTGACTCCAGAGAAACGGCCCTCGGGCATGTTCCATTCCTCGGTTCTGTGCGAGTGTAT	3288
Qy	2149	GTGCGCGGCGGGGCGACAGCAGGGGAGGACCTACTCTCCCGCAGGCGCGCTCTCCTACTTG	2208	Db	3241	GTGACTCCAGAGAAACGGCCCTCGGGCATGTTCCATTCCTCGGTTCTGTGCGAGTGTAT	3300
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Qy	2209	AAGGGCTTTTGGGCGGTCCACTGCTCTGCCCCCTCGGGGACGCTGCGGCACTTTTGGG	2268	Db	3301	GACCGGGCTGTGTGGTACGAGCTCAACGCGCGGAGAGACCTCAGTTAGTTGCGGGCT	3360
Db	2221	AAGGGCTTTTGGGCGGTCCACTGCTCTGCCCCCTCGGGGACGCTGCGGCACTTTTGGG	2280	Qy	3349	TACCTTAACACACAGAGGTTGCCGCTGTGCCAGAGACCTCTGGAGTTCTGGGAGAGGCTC	3408
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Qy	2329	GAACACACTATGCGGTCCCGGTCTTACGAGACAACTCGTCCCTCGGCGGTACCGGAG	2388	Db	3421	TTTACAGGCTTACCCACATAGAGCGCCATTTCTTGTCCCAGACTAAGACGAGGAGGAGAC	3480
Db	2341	GAACACACTATGCGGTCCCGGTCTTACGAGACAACTCGTCCCTCGGCGGTACCGGAG	2400	Qy	3469	AACTTCCCTTACCTGGTAGCATACAGGCTACGCTGTGCGGCGAGGCTCAGGCTCCACCT	3528
Qy	2389	ACATTCAGGTGGCCCACTTACAGCGCCCTTACTGCTAGCGGCAAGAGCACTAAGGTGCGG	2448	Db	3481	AACTTCCCTTACCTGGTAGCATACAGGCTACGCTGTGCGGCGAGGCTCAGGCTCCACCT	3540
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Qy	2449	GCTGCGTATGACGCGCAAGGATTAAGGTGCTTGTCTGAACCGCTCGTGCAGCGCCACC	2508	Db	3541	CCATGCTGGGACCAAAATGTGGAAGTGTCTATACGCTTAAGCCTACGCTGCGAGGCGCA	3600
Db	2461	GCTGCGTATGACGCGCAAGGATTAAGGTGCTTGTCTGAACCGCTCGTGCAGCGCCACC	2520	Qy	3589	ACGCCCCCTGTGTATAGGCTGGGAGCGGTTCCAAAACGAGGTTACTACACACACCCCAT	3648
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Db	2521	CTAGGTTTCCGGGGGTATATGCTTAAGGCACATGCTATCGACCTTAACATCAGAACCGGG	2580	Qy	3649	ACCAATATCATCATGCGCATGCTGCGCTGACCTCGGAGGTCGTCAAGAGCACTGGGTG	3708
Qy	2569	GTAAGGACCATACACAGGGTGCCTCCCATACGTAAGTCTTCCATATGGCAAGTTTCTGGC	2628	Db	3661	ACCAATATCATCATGCGCATGCTGCGCTGACCTCGGAGGTCGTCAAGAGCACTGGGTG	3720
Db	2581	GTAAGGACCATACACAGGGTGCCTCCCATACGTAAGTCTTCCATATGGCAAGTTTCTGGC	2640	Qy	3709	CTGCTAGCGGAGTCTTAGCAGCTCTGCGCGGTATTGCTGCAACAGGAGGAGGAGGAGG	3768
Qy	2629	GACGGTGGTGTCTCTGGGGCGCTATGACATCATATATGATGATGAGTGCACCTCACT	2688	Db	3721	CTGCTAGCGGAGTCTTAGCAGCTCTGCGCGGTATTGCTGCAACAGGAGGAGGAGGAGG	3780
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Db	2701	GACTCGACCACTATCTCTGGGATCGGACAGTCTCTGGACCAAGCGGAGAGCGGCTGGAGCG	2760	Qy	3829	TACCGGAGTTCGATGAGATGGAGAGTGGCGCTCACACCTTCTTATATCGAAACAGGGA	3888
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Db	2761	CGACTCGTGTGCTGCGCACCGCTACGCTCTCGGGATCGGTCAACGCTGCCACATCCAAAC	2820	Qy	3889	ATGCGAGCTCGCGCAACAAATTCAAACAGAGGCAATCGGGTGTCTGCAACAGCCACCAAG	3948
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Qy	7549	AAGTACCTCTTCAACTGGGCGAGTAAGGACCAAGCTCAAATCTCACTCCAAATCCCGGCTGCG	7608
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Qy	7669	AGCTGTCTCGTGCCTCCAGCCCGCTGGTTTCATGTGTGGTGCCTTACTCTTCTGTAGGG	7728
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LOCUS	Sequence 28 from patent US 6630343.		linear
DEFINITION	Sequence 28 from patent US 6630343.		
ACCESSION	AR406049		
VERSION	AR406049.1	GI:40155176	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 8001)		
AUTHORS	Bartenschlager,R.		
TITLE	Hepatitis C virus culture system		
JOURNAL	Patent: US 6630343-A 28 07-OCT-2003;		
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Query Match	99.3%	Score 7935;	DB 6; Length 8001;

Best Local Similarity 99.6%; Pred. No. 0; Matches 7969; Conservative 0; Mismatches 20; Indels 12; Gaps 1;			
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QY	241	GGGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGGCTTGTGTACTGTGCTGATAGG	300
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QY	1069	TTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCTGTCCTTACGGTATCGCGG	1128
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Db	1141	CTCCCGATTTCGAGCGCATCGGCTTCTATCGCCTTCTTACGAGTTCCTCTGAGTTTAA	1200
QY	1189	CAGACCAACAGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCT	1248
Db	1201	CAGACCAACAGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCT	1260
QY	1249	AAGCTTACTGGCGGAAGCGCTTGGAAATAGGCGGCTGTCGTTCTCTATATGTTATTT	1308
Db	1261	AAGCTTACTGGCGGAAGCGCTTGGAAATAGGCGGCTGTCGTTCTCTATATGTTATTT	1320
QY	1309	TCCACCATATTCGCTTCTTGGCAATGAGGGCCCGGAAACCTGGCCCTCTCTCTCTG	1368
Db	1321	TCCACCATATTCGCTTCTTGGCAATGAGGGCCCGGAAACCTGGCCCTCTCTCTCTG	1380
QY	1369	ACGAGCTTCTAGGGGCTTCTTCCCTCTCGCAAGGAATGCAAGCTCTGTGTAATGTC	1428
Db	1381	ACGAGCTTCTAGGGGCTTCTTCCCTCTCGCAAGGAATGCAAGCTCTGTGTAATGTC	1440
QY	1429	GTGAAGGAGCAGTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGCTCTGTAGGACCTTT	1488
Db	1441	GTGAAGGAGCAGTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGCTCTGTAGGACCTTT	1500
QY	1489	TGCAGGACGGAACCCCGCTCTGCGACAGTGCCTCTGCGGCCCAAGACAGCTGTA	1548
Db	1501	TGCAGGACGGAACCCCGCTCTGCGACAGTGCCTCTGCGGCCCAAGACAGCTGTA	1560
QY	1549	TAAGATACACTGCAAGGCGGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGTG	1608
Db	1561	TAAGATACACTGCAAGGCGGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGTG	1620
QY	1609	GAAGAGTCAATGCTCTCCTCAAGCTATTCAACAGGGGCTGAAGATGCCAGAG	1668
Db	1621	GAAGAGTCAATGCTCTCCTCAAGCTATTCAACAGGGGCTGAAGATGCCAGAG	1680
QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGCTCTGGTGCACATGTTTACATGTTTATG	1728
Db	1681	GTACCCCATTTGATGGGATCTGATCTGGGCTCTGGTGCACATGTTTACATGTTTATG	1740
QY	1729	TCGAGGTTAAAAAAGCTCTAGGCCCGCCGAAACACAGGGGACGTGTTTTCTTTGAAAA	1788
Db	1741	TCGAGGTTAAAAAAGCTCTAGGCCCGCCGAAACACAGGGGACGTGTTTTCTTTGAAAA	1800
QY	1789	CACGATATACATGCGGCTTACAGGCTTACTTCCCAACAGACGCGAGGCTACTTGGC	1848
Db	1801	CACGATATACATGCGGCTTACAGGCTTACTTCCCAACAGACGCGAGGCTACTTGGC	1860
QY	1849	TGCATCATCACTAGCTTCAAGGCGGACAGGAACACAGGTCGAGGGGAGGTCCAGGTG	1908
Db	1861	TGCATCATCACTAGCTTCAAGGCGGACAGGAACACAGGTCGAGGGGAGGTCCAGGTG	1920
QY	1909	GTCTCCACCGCAACAAATCTTTCTGCGGACCTGCTGCTCAATGCGCTGTGTTGACTGTC	1968
Db	1921	GTCTCCACCGCAACAAATCTTTCTGCGGACCTGCTGCTCAATGCGCTGTGTTGACTGTC	1980
QY	1969	TATCATGTGCGGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCACCAATGATC	2028
Db	1981	TATCATGTGCGGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCACCAATGATC	2040
QY	2029	ACCAATGFGACAGGACCTCTGTCGGTGGCAAGCGCCCGCGGGCGCTTCTTGTGACA	2088
Db	2041	ACCAATGFGACAGGACCTCTGTCGGTGGCAAGCGCCCGCGGGCGCTTCTTGTGACA	2100
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QY 2149 GTGCGCGGCGGCGGAGACAGCAGGAGGAGGCTACTCTCCCGCAGGCCGCTCTCTACTTG 2208
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QY 2209 AAGGGCTCTTCGGCGGCTCCACTGCTCTGCCCTCGGGGCAAGCTGTGGGCATCTTTCCG 2268
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Db 2281 GCTGCCGTGTGACCCCGAGGGGTTCGAAGGCGGTGGAATTTGTACCCGCTGAGTCTATG 2340
QY 2329 GAACAACATATGCGGTCCCGCTCTTCAAGGCAACTCTGCTCCCTCGGCGGTACCCGAG 2388
Db 2341 GGAACCACTATGCGGTCCCGCTCTTCAAGGCAACTCTGCTCCCTCGGCGGTACCCGAG 2400
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Db 2401 ACATTCAGGTGGCCCATCTACAGCCCTACTGCTAGCGCAAGAGCACTAAGGTGCG 2460
QY 2449 GCTGCGTATGACGCCCAAGGATTAAGGTGCTTGTCTGAAACCCGCTCGCGGCCAACC 2508
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QY 2509 CTAGTTTCGGGGCGGTATATGTCTTAAGGCAATGGTATCGACCCCTAACATCAGAATCGG 2568
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QY 3529 CCATCTGGGACCAATGTGGAAGTGTCTCATACGGCTAAGCCTACGCTGCAGCGGCCA 3588
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Db 4261 ATAGCCTTGGAGAGGCTGTGTGATATTTTGGCAGGTTATGAGCAGGGGTGCGAGC 4320
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DB	6601	TTCCTGTGTGAATGCTGTGAAAGCGAAGAAATGCCCTATGGGCTTCGGCATATGACACCCGC	6660
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DB	6661	TGTTTTGACTCAACGGTCACTGAGATGACATCCGTGTGAGGAGTCAATCTTACCAATGT	6720
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QY	6769	GGGGGCCCCCTGACTAATTTCTAAAGGCGAGAACTTCGGGCTATCCCGGTGCCCGCGGAGC	6828
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QY	6829	GGTGTACTGACGACCGAGCTGGGTAAATACCTTCACATTTACTTTGAAGGCGGCTTCGGGCC	6888
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DB	6901	TGTCGAGCTGCGAAGCTCCAGGACTGCAACGATGCTCGTATGCCGAGACGACCTTTGCTTT	6960
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DB	6961	ATCTGTGAAAGCGGGGAGCCCAAGAGGACGAGCGAGCCTACCGGCCTTTCACGAGGCT	7020
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DB	7321	CTAGATTGTGAGATCTACGGGGCTGTACTCAATTGAGCCATTGAGCCTCCTCAGATC	7380
QY	7369	ATTCAACGACTCCATGSCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATC	7428
DB	7381	ATTCAACGACTCCATGSGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATC	7440
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QY	7669	AGCCTGTCCTGTCGCCGACCCGCTGGTTCATGTGGTGCCTACTCCCTACTCTTCTGTGAGGG	7728
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SOURCE	Hepatitis C virus		
ORGANISM	Hepatitis C virus		
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.			
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AUTHORS	Bartenschlager,R.D.		
TITLE	Hepatitis c virus cell culture system		
JOURNAL	Patent: EP 1043399-A 10 11-OCT-2000;		
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Best Local Similarity 99.6%; Pred.No. 0;			
Matches 7969; Conservative 0; Mismatches 20; Indels 12; Gaps 1;			
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QY	61	TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTCTCGTCAGCGCTCCAGGAC	120
DB	61	TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTCTCGTCAGCGCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGACCGGTGAGTACACCGGAATTGCCAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGACCGGTGAGTACACCGGAATTGCCAG	180
QY	181	GACGACCGGGTCTTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGGCGTCCCCCC	240
DB	181	GACGACCGGGTCTTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGGCGTCCCCCC	240
QY	241	GGGAGACTGTACCGAGTAGTGTGTTGGGTCCGAAAGCCCTTGTGCTACTGCTGATAGG	300

Db 241 GCGAGACTCTAGCCAGTAGTGTGGTTCGGAAGGCTGTGGTACTGCTGATAGG 300
Qy 301 GTGCTTGCAGTGCCTCCGCGGAGTCTCTGAGACCGTGCACATGAGCAGCAATCTTAAC 360
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Qy 361 CTCGAAGAAACCAAA-----GGGGCGCCCATGATTGACAGATGGATTGC 408
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Qy 409 AGCGAGTTCTCCGCGCGCTTGGTGCAGAGGCTATTGCGCTATGACTGGGCACACAGA 468
Db 421 AGCGAGTTCTCCGCGCGCTTGGTGCAGAGGCTATTGCGCTATGACTGGGCACACAGA 480
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Db 541 TTGTCAGACCGACTGTCCGGTGCCTGATGAATGAATGAGACGAGGAGCGCGCTAT 600
Qy 589 CGTGGCTGGCCACGACGCGGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGG 648
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Qy 649 GAAGGACTGGCTGCTATTGGGCGAAGTCCGGGCGAGGATCTCTGTCACTCACTTGT 708
Db 661 GAAGGACTGGCTGCTATTGGGCGAAGTCCGGGCGAGGATCTCTGTCACTCACTTGT 720
Qy 709 CTCTGCGGAGAAAGTATCCATATGCGCTGATGCAATGCGCGCGCTGCATACGTTGATC 768
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Qy 769 CGGCTACTGCCATTCGACACCAAGCGAAACATCGCATCGAGCGAGCACTCGGA 828
Db 781 CGGCTACTGCCATTCGACACCAAGCGAAACATCGCATCGAGCGAGCACTCGGA 840
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Db 841 TGAAGCCGCTCTTGTGATGAGATGATCTGGAAGAGAGCATCAGGGGCTCGCGCAG 900
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Db 901 CCGAATCTTTCGCGAGCTCAAGCGCGCATGCCCGAGCGAGGATCTGTCGTGACCC 960
Qy 949 ATGCGGATGCTGCTTCCGAATATCATGTGGAATAATGGCGGCTTTCTGGAATCATCG 1008
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Db 1081 TTGCTGAGAGCTTGGCGCGCAATGGCTGACCGCTTCTGCTTTTACGGTATCGCG 1140
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Qy 1429 GTGAAGGAGCAGTTCCTCTGGAAGCTTCTTGAAGCAAAACACGCTCTGTAGCGACCTT 1488
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Qy 1489 TGCAGCAGCGAAACCCCCCACTTGGCGACAGGTGCTCTGGCGCAAAAGCCACCTGTA 1548
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Qy 1549 TAAGATACACCTGCAAGGCGCAAAACCCCACTTGGCGACAGGTGCTGTGAGTGTGATGTTG 1608
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Qy 1609 GAAAGAGTCAAAATGGCTCTCTCAAGCTATTCAACAGGGGCTGAAGGATGCCAGAAG 1668
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Qy 1909 GTCTCCACCGCAACAAATCTTTCTGGCGACCTGCGTCAATGGCGTGTGTGGACTGTC 1968
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Db 1981 TATCATGGTGGCGCTCAAAAGACCTTTGCGGCGCCAAAGGCGCCCAATCAACCAATGTAC 2040
Qy 2029 ACCAATGTGACAGGACCTCTGCGGTGCAAGCGCCCGCGGGCGCGTTCCTTGACA 2088
Db 2041 ACCAATGTGACAGGACCTCTGCGGTGCAAGCGCCCGCGGGCGCGTTCCTTGACA 2100
Qy 2089 CCATGCACTTGGCGAGCTCGGACCTTTTACTTGTGTACAGGGCATGCCGATGCTATCCG 2148
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Qy 2149 GTGCGCGCGGGGCGAGCAGAGGGGAGCTTCTCTCCCGAGGCGCTCTCTACTTTG 2208
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Qy 2209 AAGGGCTTTCGGGCGGTTCACCTCTGCGCGCTCGGGGACGCTGTGGGCACTCTTCGG 2268
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Qy 2269 GCTGCCGTGTGACCCGAGGGGTTGCAAGGCGGTGGAATTTGTACCGCTGAGTCTATG 2328
Db 2281 GCTGCCGTGTGACCCGAGGGGTTGCAAGGCGGTGGAATTTGTACCGCTGAGTCTATG 2340
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Db 2341 GAAACCAATATGCGGTTCGCGGTCTTTCACGAGCAACTCGTCCCTCCGCGGTACCGGAG 2400
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[illegible]

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Qy	7969	TGGCTCT	CTGCA	TCAAGT	7989																		
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AR406041																							
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ACCESSION	AR406041																						
VERSION	AR406041.1																						
KEYWORDS	1. GI:40155168																						
SOURCE	Unknown.																						
ORGANISM	Unknown.																						
REFERENCE	Unclassified.																						
AUTHORS	1 (bases 1 to 8637)																						
TITLE	Bartenschlager, R.																						
JOURNAL	Hepatitis C virus culture system																						
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Db	1	GCCAGCCCCG	ATTGGGGCG	CACCTCC	ACCATTAG	ATCACTCCC	CTGTGAGG	AACTACTG				60											
Qy	61	TCCTCAGC	AGAAAGCGT	CTAGCCAT	GGCGTTAGT	ATAGTGTCTG	CGACGCCTCC	AGGAC				120											
Db	61	TCCTCAGC	AGAAAGCGT	CTAGCCAT	GGCGTTAGT	ATAGTGTCTG	CGACGCCTCC	AGGAC				120											
Qy	121	CCCCCTCC	CGGAGAGCC	ATAGTGTCTG	CGAACCGGTG	AGTACACCG	GAATTGCC	AG				180											
Db	121	CCCCCTCC	CGGAGAGCC	ATAGTGTCTG	CGAACCGGTG	AGTACACCG	GAATTGCC	AG				180											
Qy	181	GACGAC	CGGCTCTT	CTTTGGAT	CAACCCGCTCA	ATGCTG	CGAGATTGG	CGGTCCCC				240											
Db	181	GACGAC	CGGCTCTT	CTTTGGAT	CAACCCGCTCA	ATGCTG	CGAGATTGG	CGGTCCCC				240											
Qy	241	GCAGACTC	TGACCGC	AGTAGTGT	TGGTTCG	CGAAAGCCCTT	GTGGTACT	CGCTGTAT	AG			300											
Db	241	GCAGACTC	TGACCGC	AGTAGTGT	TGGTTCG	CGAAAGCCCTT	GTGGTACT	CGCTGTAT	AG			300											
Qy	301	GTGCTT	GCAGTGCC	CGGAGGTCT	GTAGACCG	TGCAACAT	G																

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Db	601	CGAGCGGCGTTCCTTGGCGAGCTGTGTCTCGACGTTGTCTGTAAGCGGGAAGGACTGGC	660
QY	661	TGCTATTGGCGAAGTCCCGGGGAGGATCTCTGTCTCATCTCACCTTGTCTCTCGCGAGA	720
Db	661	TGCTATTGGCGAAGTCCCGGGGAGGATCTCTGTCTCATCTCACCTTGTCTCTCGCGAGA	720
QY	721	AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCAATGCGCTTGTATCGGCTACCTGCC	780
Db	721	AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCAATGCGCTTGTATCGGCTACCTGCC	780
QY	781	CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGGACGTAAGTGAAGCGCGTC	840
Db	781	CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGGACGTAAGTGAAGCGCGTC	840
QY	841	TTGTGATCAGATGATCTGACGAGAGCATCAGGGGCTCGCGCCGATGCTTGGTTCG	900
Db	841	TTGTGATCAGATGATCTGACGAGAGCATCAGGGGCTCGCGCCGATGCTTGGTTCG	900
QY	901	CCAGGCTCAAGCGGCGCATGCGCCGAGGATCTCGTGTGACCATGCGGATGCTT	960
Db	901	CCAGGCTCAAGCGGCGCATGCGCCGAGGATCTCGTGTGACCATGCGGATGCTT	960
QY	961	GCTTCCGGAATATCATGTGGAATAATGCGCGCTTCTGGATTTCAGCTGTCGCGCGC	1020
Db	961	GCTTCCGGAATATCATGTGGAATAATGCGCGCTTCTGGATTTCAGCTGTCGCGCGC	1020
QY	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCTGTGCTACCGTGTATTTGTGAAGAGC	1080
Db	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCTGTGCTACCGTGTATTTGTGAAGAGC	1080
QY	1081	TTGGCGGGAATGCGGCTGACCGCTTCTCGTGTGTTACCGTATCGCGCTTCCGATTCG	1140
Db	1081	TTGGCGGGAATGCGGCTGACCGCTTCTCGTGTGTTACCGTATCGCGCTTCCGATTCG	1140
QY	1141	AGCGCATCGCTTCTATPCCGCTTCTTTCAGAGTTCCTTCTGAGTTTAAACAGACCAACG	1200
Db	1141	AGCGCATCGCTTCTATPCCGCTTCTTTCAGAGTTCCTTCTGAGTTTAAACAGACCAACG	1200
QY	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTTACTGGC	1260
Db	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTTACTGGC	1260
QY	1261	CGAAGCGCTTGAATAAGGCGGCTGTGCTTGTCTATATGTTATTTTCCACCATATTG	1320
Db	1261	CGAAGCGCTTGAATAAGGCGGCTGTGCTTGTCTATATGTTATTTTCCACCATATTG	1320
QY	1321	CCGTCTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTCTTCTTTCAGGACGATTCCT	1380
Db	1321	CCGTCTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTCTTCTTTCAGGACGATTCCT	1380
QY	1381	AGGGCTTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGTAATGTTTCTGAAAGCA	1440
Db	1381	AGGGCTTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGTAATGTTTCTGAAAGCA	1440
QY	1441	GTTCCTCTGGAAGCTTCTTGAAGACAAACAAAGTCTGTAGGACCTTTGACGAGCGG	1500
Db	1441	GTTCCTCTGGAAGCTTCTTGAAGACAAACAAAGTCTGTAGGACCTTTGACGAGCGG	1500
QY	1501	AACCCCGCATCTGGCGACAGTGTCTGTGGCGGAAAGCCAGCTGTATAGATACACT	1560
Db	1501	AACCCCGCATCTGGCGACAGTGTCTGTGGCGGAAAGCCAGCTGTATAGATACACT	1560
QY	1561	GCAAGGCGGCAACCCAGTGTGCGGCGGAAAGCCAGCTGTATAGATACACT	1620
Db	1561	GCAAGGCGGCAACCCAGTGTGCGGCGGAAAGCCAGCTGTATAGATACACT	1620
QY	1621	TGGCTCTCTCAAGGATTTCAAAGGGCTGAGGATGCCAGAGGTACCCCATTTG	1680
Db	1621	TGGCTCTCTCAAGGATTTCAAAGGGCTGAGGATGCCAGAGGTACCCCATTTG	1680
QY	1681	ATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTTACATGTGTTTGTAGTCGAGGTTAAAA	1740

Db	1681	ATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTTACATGTGTTTGTAGTCAGGTTAAAA	1740
QY	1741	AAGTCTTAGGCGCCCGGAAACACGCGGACGCTGTTTCTTTTGAAGAAACAGATATACC	1800
Db	1741	AAGTCTTAGGCGCCCGGAAACACGCGGACGCTGTTTCTTTTGAAGAAACAGATATACC	1800
QY	1801	ATG-----	1803
Db	1801	ATGACCGGAGATGGCAGCATCGTGGAGCGGTTTTCGTAGTCTGATATCTTTG	1860
QY	1804	-----	1803
Db	1861	ACCTTGTACCGCACTATAAGCTGTTCTCTGCTAGGCTCATATGTTGTTTACATATTTT	1920
QY	1804	-----	1803
Db	1921	ATCACCAGGCGGAGGACACCTTGCNAAGTGGATCCCCCCTCAACGTTCCGGGGGCG	1980
QY	1804	-----	1803
Db	1981	CGCGATGCGGTATCTCTCTCACGTGCGGATCCACCAGAGCTAATCTTTACCATCACC	2040
QY	1804	-----	1803
Db	2041	AAATCTTTGCTGCCATATCTCGTCCACTCATGTGCTCCAGGCTGTTATACCAAGATG	2100
QY	1804	-----	1803
Db	2101	CCGTACTCTGTCGCGCACACGGGCTCATTCGTGATGATGCTGTGCGGAAGTTGCT	2160
QY	1804	-----	1803
Db	2161	GGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTTGGCCGCTGACAGGTACGTACGTT	2220
QY	1804	-----	1803
Db	2221	TATGACCATCTCAACCACTGGGCGGACCTGGCCCGGCTTACGAGACCTTGGGCTG	2280
QY	1804	-----	1803
Db	2281	GCAGTTGAGCCGCTGCTTCTCTGATATGAGACCAAGTTATCACCTGGGGGCGAGAC	2340
QY	1804	-----	1803
Db	2341	ACCGCGCGTGTGGGACATCATCTTTGGGCTTCCCGCTCTCCCGCGCGGGGAGGAG	2400
QY	1804	-----	1812
Db	2401	ATACATCTGGGACCGGCGAGACGCTTGAAGGCGAGGGTGGCGACTCTCTCGCGCTATT	2460
QY	1813	ACGGCTTACTTCCCAACAGACGCGAGGCTTACTTGGGTGATCATCATCTAGCTCACAGGC	1872
Db	2461	ACGGCTTACTTCCCAACAGACGCGAGGCTTACTTGGGTGATCATCATCTAGCTCACAGGC	2520
QY	1873	CGGACAGGAACAGAGTGTGAGGGGAGGTCAGGTGCTTCCCGCAACACATCTTTC	1932
Db	2521	CGGACAGGAACAGAGTGTGAGGGGAGGTCAGGTGCTTCCCGCAACACATCTTTC	2580
QY	1933	CTGGGACCTGCGTCAATGGCTGTGTGGACTGTCTATCATGTGCGGCTCAAGAC	1992
Db	2581	CTGGGACCTGCGTCAATGGCTGTGTGGACTGTCTATCATGTGCGGCTCAAGAC	2640
QY	1993	CTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	2052
Db	2641	CTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	2700
QY	2053	GGTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	2112
Db	2701	GGTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	2760
QY	2113	CTTTACTTGGTTCACGAGGATGCGGATGTCATTCGGTGGCGGCGGCGGCGGCGGCGGCGG	2172

2761	DB	CTTTACTTTGGTCACGAGGCATGCGCATGTCAATTCGGCTGCGCGCGGGCGACAGCAGG	2820
2173	QY	GGGAGCCTACTCTCTCCCGACGCCGCTCTCCTACTTTGAAGGCTCTTCGCGGGGTTCACTG	2232
2821	DB	GGGAGCCTACTCTCTCCCGACGCCGCTCTCCTACTTTGAAGGCTCTTCGCGGGGTTCACTG	2880
2233	QY	CTCTGCCCCCTCGGGGCAACGCTGTGGGCATCTTTTCGGGCTGCGGTGTGCACCCCGAGGGTT	2292
2881	DB	CTCTGCCCCCTCGGGGCAACGCTGTGGGCATCTTTTCGGGCTGCGGTGTGCACCCCGAGGGTT	2940
2293	QY	GCGAAGCGGGTGAGACTTTGTACCCGTCGAGTCTATGGAACCACTATGCGGTCTCCCGGTC	2352
2941	DB	GCGAAGCGGGTGAGACTTTGTACCCGTCGAGTCTATGGAACCACTATGCGGTCTCCCGGTC	3000
2353	QY	TTCACGGACAACCTCGTCCCCCTCGCGCGTACCGCAGACATTTCCAGGTGGCCCATCTACAC	2412
3001	DB	TTCACGGACAACCTCGTCCCCCTCGCGCGTACCGCAGACATTTCCAGGTGGCCCATCTACAC	3060
2413	QY	GCCCCCTACTGGTAGCGCAAGACACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGGTAT	2472
3061	DB	GCCCCCTACTGGTAGCGCAAGACACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGGTAT	3120
2473	QY	AAGGTGCTTGTCCCTGAACCGTCCGTGCGCGCAACCTTAGGTTTCGGGCGTATATGCT	2532
3121	DB	AAGGTGCTTGTCCCTGAACCGTCCGTGCGCGCAACCTTAGGTTTCGGGCGTATATGCT	3180
2533	QY	AAGGCACATGGTATCGACCTTAACATCAGAAACCGGGTAAGACCATCACACGGGTGCC	2592
3181	DB	AAGGCACATGGTATCGACCTTAACATCAGAAACCGGGTAAGACCATCACACGGGTGCC	3240
2593	QY	CCCATCAGTACTCCACTATGGCAAGTTTCTTGCAGCGGTGGTGTCTTGGGGGCGCC	2652
3241	DB	CCCATCAGTACTCCACTATGGCAAGTTTCTTGCAGCGGTGGTGTCTTGGGGGCGCC	3300
2653	QY	TATGACATCATAAATATGTGATCAGTGCCCACTCACTGACTGCACCATCTATCTGGGCATC	2712
3301	DB	TATGACATCATAAATATGTGATCAGTGCCCACTCACTGACTGCACCATCTATCTGGGCATC	3360
2713	QY	GGCACAGTCTTGGACCAAGCGGAGACGGCTGGAGCGGACTCTGCTGCTCGCACCGCT	2772
3361	DB	GGCACAGTCTTGGACCAAGCGGAGACGGCTGGAGCGGACTCTGCTGCTCGCACCGCT	3420
2773	QY	ACGCTCCGGGATCGGTACCGTGGCAATCCAAACATCGAGGAGTGGCTCTCTCCAGC	2832
3421	DB	ACGCTCCGGGATCGGTACCGTGGCAATCCAAACATCGAGGAGTGGCTCTCTCCAGC	3480
2833	QY	ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	2892
3481	DB	ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	3540
2893	QY	CACCTCATTTTCTGCCATTTCCAAAGAAATGTGATGAGCTCGCGCGAAGCTGTCCGGC	2952
3541	DB	CACCTCATTTTCTGCCATTTCCAAAGAAATGTGATGAGCTCGCGCGAAGCTGTCCGGC	3600
2953	QY	CTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGATGTATCGTGCATACCAACTAGC	3012
3601	DB	CTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGATGTATCGTGCATACCAACTAGC	3660
3013	QY	GGAGACGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGCGATTTGAC	3072
3661	DB	GGAGACGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGCGATTTGAC	3720
3073	QY	TCAGTGTATCGACTGCAATAATGTGTACCAGACAGTTCGACTTCAGCTTGAGCCCGACC	3132
3721	DB	TCAGTGTATCGACTGCAATAATGTGTACCAGACAGTTCGACTTCAGCTTGAGCCCGACC	3780
3133	QY	TTCAACATTGAGACGACGCGGTGCCAAGACGCGGTGTCACTTCGACGCGGCGAGGC	3192
3781	DB	TTCAACATTGAGACGACGCGGTGCCAAGACGCGGTGTCACTTCGACGCGGCGAGGC	3840
3193	QY	AGGACTGGTAGGGGCAAGATGGGCATTTTACAGGTTTGTGACTCCAGGAAACGGCCCTCG	3252
3841	DB	AGGACTGGTAGGGGCAAGATGGGCATTTTACAGGTTTGTGACTCCAGGAAACGGCCCTCG	3900

QY	3253	GGCATGTTTCGATTCTCTCGGTTCTGTGCGAGTGTCTATGACGCGGGCTGTGCTTGGTACGAG	3312
Db	3901	GGCATGTTTCGATTCTCTCGGTTCTGTGCGAGTGTCTATGACGCGGGCTGTGCTTGGTACGAG	3960
QY	3313	CTCAGCGCGCGGAGACCTTCAGTTTAGGTTGCGGGCTTACCTAAACACACACGAGGTTGCCCC	3372
Db	3961	CTCAGCGCGCGGAGACCTTCAGTTTAGGTTGCGGGCTTACCTAAACACACACGAGGTTGCCCC	4020
QY	3373	GTCTGCCAGGACCACTCTCGAGTTCTGGGAGAGGCTTTTACAGGCCCTCAACCCACATAGAC	3432
Db	4021	GTCTGCCAGGACCACTCTCGAGTTCTGGGAGAGGCTTTTACAGGCCCTCAACCCACATAGAC	4080
QY	3433	GCCCATTTCTGTCCCAGACTAAGCAGCAGCAGAGACAACCTTCCCTCTACCTGCTAGCATAC	3492
Db	4081	GCCCATTTCTGTCCCAGACTAAGCAGCAGCAGAGACAACCTTCCCTCTACCTGCTAGCATAC	4140
QY	3493	CAGGCTACGTTGTGGCGCAGGGCTCAGGCTCCACTCCATCGTGGGACCAAAATGTGGAAG	3552
Db	4141	CAGGCTACGTTGTGGCGCAGGGCTCAGGCTCCACTCCATCGTGGGACCAAAATGTGGAAG	4200
QY	3553	TGTCCTATACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCTCTGCTGTATAGGCTGGGA	3612
Db	4201	TGTCCTATA CGGCTTAAGCCTTACGCTGCACGGGCCAACGCCCTCTGCTGTATAGGCTGGGA	4260
QY	3613	GCCGTTCAAAACGAGGTTACTTACCACACACCCCATAACCAATATACATGCGCATGCAATG	3672
Db	4261	GCCGTTCAAAACGAGGTTACTTACCACACACCCCATAACCAATATACATGCGCATGCAATG	4320
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Db	4621	GTGGAATCAAGTGGCGGACCTTCGAAGACCTTCTGGGCGAAGCATATGTGGAATTCATC	4680
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QY	4273	GATATTTTGGCAGGTTATGGAGCAGGGTGTGACGGCGCTCGTGGCTTTAAGTCAATG	4332
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DEFINITION Sequence 2 from Patent EP1043399.
ACCESSION AX036253
VERSION AX036253.1 GI:11225869
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE
1 Bartenschlager R.D.
AUTHORS Hepatitis C virus cell culture system
TITLE Patent: EP 1043399-A 2 11-OCT-2000;
JOURNAL BARTENSCHLAGER RAUF DR (DE)
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ORIGIN

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QY	1933	CTGGGACCTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTCCGGCTCAAGACC	1992
Db	2581	CTGGGACCTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTCCGGCTCAAGACC	2640
QY	1993	CTTGGCGGCGCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGACAGGACTCGTC	2052
Db	2641	CTTGGCGGCGCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGACAGGACTCGTC	2700
QY	2053	GGCTGGCAAGCCCGCCCGGGCGGCTTCTTTGACACCAATGACCTTGGCGAGCTCGGAC	2112
Db	2701	GGCTGGCAAGCCCGCCCGGGCGGCTTCTTTGACACCAATGACCTTGGCGAGCTCGGAC	2760
QY	2113	CTTTACTTGGTACAGAGGATGCGGATGTCAATTCGGGTGCGCGGCGGACAGCAGG	2172
Db	2761	CTTTACTTGGTACAGAGGATGCGGATGTCAATTCGGGTGCGCGGCGGACAGCAGG	2820
QY	2173	GGGAGCTACTCTCCCGCAGGCGCTCTCTACTTGAAGGGCTCTTCCGGCGGTCCACTG	2232
Db	2821	GGGAGCTACTCTCCCGCAGGCGCTCTCTACTTGAAGGGCTCTTCCGGCGGTCCACTG	2880
QY	2233	CTCTGCCCTCGGGCAGCCTGTGGGCATCTTTCCGGCTGCGCTGTGACCCCGAGGGGT	2292
Db	2881	CTCTGCCCTCGGGCAGCCTGTGGGCATCTTTCCGGCTGCGCTGTGACCCCGAGGGGT	2940
QY	2293	GCGAAGGGGTGGATTTGTACCGTGTGAGTCTATGGAACCACTATGCGGTCCCGGTC	2352
Db	2941	GCGAAGGGGTGGATTTGTACCGTGTGAGTCTATGGAACCACTATGCGGTCCCGGTC	3000
QY	2353	TTACAGGACAACTCGTCCCTCCGCGCGTACCGAGCATTTCCAGGTGGGCCATCTACAC	2412
Db	3001	TTACAGGACAACTCGTCCCTCCGCGCGTACCGAGCATTTCCAGGTGGGCCATCTACAC	3060
QY	2413	GCCCTACTGGTAGCGCAAGACACTAAGGTGCGCGCTGGTATGAGGCCCAAGGGTAT	2472
Db	3061	GCCCTACTGGTAGCGCAAGACACTAAGGTGCGCGCTGGTATGAGGCCCAAGGGTAT	3120
QY	2473	AAGGTGCTTCTGTAACCGCTGCTGCGCGCACCCCTAGGTTCGGGGGCTATATGCT	2532
Db	3121	AAGGTGCTTCTGTAACCGCTGCTGCGCGCACCCCTAGGTTCGGGGGCTATATGCT	3180
QY	2533	AAGGCACATGGTATCGAACCTTAACATCAGAACCGGGGTAAAGGACCATCAACCGGTGCC	2592
Db	3181	AAGGCACATGGTATCGAACCTTAACATCAGAACCGGGGTAAAGGACCATCAACCGGTGCC	3240
QY	2593	CCCATCAGTATCCACCTATGGCAAGTTTCTTGGCGACGGTGGTGTCTTGGGGGCGCC	2652
Db	3241	CCCATCAGTATCCACCTATGGCAAGTTTCTTGGCGACGGTGGTGTCTTGGGGGCGCC	3300
QY	2653	TATGACATCAATATGTGATGTGCTGCTCACTCACTGACCTGACCTATCTTGGGCATC	2712
Db	3301	TATGACATCAATATGTGATGTGCTGCTCACTCACTGACCTGACCTATCTTGGGCATC	3360
QY	2713	GGCAGAGTCCCTGGACCAAGCGGAGCGGTGGAGCGGACTCGTGTGTGGCCACCGCT	2772
Db	3361	GGCAGAGTCCCTGGACCAAGCGGAGCGGTGGAGCGGACTCGTGTGTGGCCACCGCT	3420
QY	2773	ACGCTCCGGATCGGTCAACCGTCCACATCCAAACATCGAGAGGTGCTCTGTCCAGC	2832
Db	3421	ACGCTCCGGATCGGTCAACCGTCCACATCCAAACATCGAGAGGTGCTCTGTCCAGC	3480
QY	2833	ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	2892
Db	3481	ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	3540
QY	2893	CACCTCATTTTCTGCAATTCGAAGAGAAATGTGATGAGCTCGCGCGAAGCTGTCCGCG	2952
Db	3541	CACCTCATTTTCTGCAATTCGAAGAGAAATGTGATGAGCTCGCGCGAAGCTGTCCGCG	3600
QY	2953	CTCGGACTCAATGTGTAGCATATTAACCGGGGCTTGTATGCCCTCATACCACTAGC	3012
Db	3601	CTCGGACTCAATGTGTAGCATATTAACCGGGGCTTGTATGCCCTCATACCACTAGC	3660
QY	3013	GGAGAGCTCAATGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGGCGATTCGAC	3072
Db	3661	GGAGAGCTCAATGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGGCGATTCGAC	3720
QY	3073	TCAGTGATCGACTCAATGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGGCGATTCGAC	3132
Db	3721	TCAGTGATCGACTCAATGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCGGCGATTCGAC	3780
QY	3133	TTACCAATTTGAGACGACGACCGCTGCCACAAGACGCGGTGTACGCTCCGAGCGGAGGC	3192
Db	3781	TTACCAATTTGAGACGACGACCGCTGCCACAAGACGCGGTGTACGCTCCGAGCGGAGGC	3840
QY	3193	AGGACTGGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTTCCAGGAGAACCGGCCCTCG	3252
Db	3841	AGGACTGGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTTCCAGGAGAACCGGCCCTCG	3900
QY	3253	GGCATGTTCCGATTTCTCGGTTCTGTGCGAGTCTATGACGGGCTGTGCTTGGTACGAG	3312
Db	3901	GGCATGTTCCGATTTCTCGGTTCTGTGCGAGTCTATGACGGGCTGTGCTTGGTACGAG	3960
QY	3313	CTACGCGCGCGGAGACCTCAAGTTAGGTTGCGGGCTTACCTAAACACACACAGGGTTGCC	3372
Db	3961	CTACGCGCGCGGAGACCTCAAGTTAGGTTGCGGGCTTACCTAAACACACACAGGGTTGCC	4020
QY	3373	GTCTGCCAGGACCAATCTGGAGTCTGGAGAGCGTCTTACAGGCTCACCCACATAGAC	3432
Db	4021	GTCTGCCAGGACCAATCTGGAGTCTGGAGAGCGTCTTACAGGCTCACCCACATAGAC	4080
QY	3433	GCCCATTTCTTGTCTCCAGACTTAAGCAGCAGGAGAGCACTTCCCTTACCTGGTAGCATAC	3492
Db	4081	GCCCATTTCTTGTCTCCAGACTTAAGCAGCAGGAGAGCACTTCCCTTACCTGGTAGCATAC	4140
QY	3493	CAGGCTACGTTGTCGCGCAGGGCTCAGGCTCCACCTCATCTGTTGGGACCAAAATGTGAG	3552
Db	4141	CAGGCTACGTTGTCGCGCAGGGCTCAGGCTCCACCTCATCTGTTGGGACCAAAATGTGAG	4200
QY	3553	TGTTCTCATACGGCTAAGCCCTAGCTGCAAGGCGCAACGCGCTTGTATAGGCTGGGA	3612
Db	4201	TGTTCTCATACGGCTAAGCCCTAGCTGCAAGGCGCAACGCGCTTGTATAGGCTGGGA	4260
QY	3613	GCGTTTCAAAAACAGAGTCTACTACACACACCCCATACCAAAATACATCATGGCATGATG	3672
Db	4261	GCGTTTCAAAAACAGAGTCTACTACACACACCCCATACCAAAATACATCATGGCATGATG	4320
QY	3673	TCGGCTGACCTGGAGTCTGTCAGAGCACCTGGGTGCTGTGTAGGCGGAGTCTCTAGCAGCT	3732
Db	4321	TCGGCTGACCTGGAGTCTGTCAGAGCACCTGGGTGCTGTGTAGGCGGAGTCTCTAGCAGCT	4380
QY	3733	CTGGGCGGCTATTTGCTGTGACCAACAGCAGCGGTGCTCAATTTGGGCGAGGATCATTTTGTCC	3792
Db	4381	CTGGGCGGCTATTTGCTGTGACCAACAGCAGCGGTGCTCAATTTGGGCGAGGATCATTTTGTCC	4440
QY	3793	GGAAAGCGCGGCTCATTTCCCGACAGGGAAGTCTTTTACCGGAGGATTCATGATGATGAA	3852
Db	4441	GGAAAGCGCGGCTCATTTCCCGACAGGGAAGTCTTTTACCGGAGGATTCATGATGATGAA	4500
QY	3853	GAGTGGGCTCAACCTCCCTTTACATCGAAACAGGGAATGACGCTCGCCGAAACAAATTCAA	3912
Db	4501	GAGTGGGCTCAACCTCCCTTTACATCGAAACAGGGAATGACGCTCGCCGAAACAAATTCAA	4560
QY	3913	CAGAGGCAATCGGGTGTGTCGCAACAGCCACCAAGCAAGCGGAGGCTGTCTCTCCGCTG	3972
Db	4561	CAGAGGCAATCGGGTGTGTCGCAACAGCCACCAAGCAAGCGGAGGCTGTCTCTCCGCTG	4620
QY	3973	GTGGAATCAAAGTGGCGGACCTCGAAGGCTTCTGGGCGAAGCATATGTGGAATTTTATC	4032
Db	4621	GTGGAATCAAAGTGGCGGACCTCGAAGGCTTCTGGGCGAAGCATATGTGGAATTTTATC	4680

QY	4033	AGCGGAGTAAATATTTAGCAGGGTTGTCCACTCTGCTGGCAACCCCGGATAGCATCA	4092	Db	5761	TTGCACAGGTACCTCTCAGCGTGCATAAACCCCTCTCTACGGAGGAGGTCAATTCCTGGTC	5820
Db	4681	AGCGGAGTAAATATTTAGCAGGGTTGTCCACTCTGCTGGCAACCCCGGATAGCATCA	4740	QY	5173	GGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATGCGAGCCCGAACCGAGCTAGCA	5232
QY	4093	CTGATGCAATTCACAGCCTCTATCACAGAGCCGCTCACACCCCAATACACCTCTCTTT	4152	Db	5821	GGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATGCGAGCCCGAACCGAGCTAGCA	5880
Db	4741	CTGATGCAATTCACAGCCTCTATCACAGAGCCGCTCACACCCCAATACACCTCTCTTT	4800	QY	5233	GTGCTCACTTCCATGTCTACCGACCCCTCCCAATTAACGGCGGAGACGGCTAAGGTAGG	5292
QY	4153	AACATCTGGGGGATGGGTGGCGGCCCAACTTCTCTCCACGGCTGTCTTGTCTTTC	4212	Db	5881	GTGCTCACTTCCATGTCTACCGACCCCTCCCAATTAACGGCGGAGACGGCTAAGGTAGG	5940
Db	4801	AACATCTGGGGGATGGGTGGCGGCCCAACTTCTCTCCACGGCTGTCTTGTCTTTC	4860	QY	5293	CTGCGCAAGGGATCTCCCCCTCTTGGCGCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	5352
QY	4213	GTAGCGCGCGCATGCGTGGAGCGGCTGTGGCAGCATAGACCTTGGAGAGTCTTGTG	4272	Db	5941	CTGCGCAAGGGATCTCCCCCTCTTGGCGCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	6000
Db	4861	GTAGCGCGCGCATGCGTGGAGCGGCTGTGGCAGCATAGACCTTGGAGAGTCTTGTG	4920	QY	5353	TCCTTGAAGGCACATGCACTTACCCGCTCATGACTCCCGCGACGCTCATTCGAGGCC	5412
QY	4273	GATATTTTGGCAGGTATGAGAGCAGGGGTGGCAGCGCGCTCGTGGCCCTTTAAGGTCA	4332	Db	6001	TCCTTGAAGGCACATGCACTTACCCGCTCATGACTCCCGCGACGCTCATTCGAGGCC	6060
Db	4921	GATATTTTGGCAGGTATGAGAGCAGGGGTGGCAGCGCGCTCGTGGCCCTTTAAGGTCA	4980	QY	5413	AACCTCTCTGTCGGCGGAGGATGGCGGGGAACATCACCCCGCTGGAGTCAAGAAATAG	5472
QY	4333	AGCGCGAGATGCCCTCCACCGAGGACCTGGCTAACTTACCTCCCTGCTATCTCTCCCT	4392	Db	6061	AACCTCTCTGTCGGCGGAGGATGGCGGGGAACATCACCCCGCTGGAGTCAAGAAATAG	6120
Db	4981	AGCGCGAGATGCCCTCCACCGAGGACCTGGCTAACTTACCTCCCTGCTATCTCTCCCT	5040	QY	5473	GTAGTAATTTTGGACTCTTTTCAGCGCTCCCAAGCGGAGGAGTGAAGAGGAAATATCC	5532
QY	4393	GGCGCCCTAGTCTCGGGTGTGTGCGCAGGATACCTGCTCGCGCAGTGGCGCCAGGG	4452	Db	6121	GTAGTAATTTTGGACTCTTTTCAGCGCTCCCAAGCGGAGGAGTGAAGAGGAAATATCC	6180
Db	5041	GGCGCCCTAGTCTCGGGTGTGTGCGCAGGATACCTGCTCGCGCAGTGGCGCCAGGG	5100	QY	5533	GTTCGGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGCA	5592
QY	4453	GAGGGGCTGTGAGTGAAGAACCGCTGATAGGCTTCCCTTCGGCGGAGTAAACACGTC	4512	Db	6181	GTTCGGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGCA	6240
Db	5101	GAGGGGCTGTGAGTGAAGAACCGCTGATAGGCTTCCCTTCGGCGGAGTAAACACGTC	5160	QY	5593	CGCCCGGATTAACACCCCTCACTGTAGAGTCTTGAAGGACCCCGACTACGCTCCCTCA	5652
QY	4513	TCCCCACACACTATGTGCTCAGACGACGCTGACGACGCTGCTGCTGCTGCTGCT	4572	Db	6241	CGCCCGGATTAACACCCCTCACTGTAGAGTCTTGAAGGACCCCGACTACGCTCCCTCA	6300
Db	5161	TCCCCACACACTATGTGCTCAGACGACGCTGACGACGCTGCTGCTGCTGCTGCT	5220	QY	5653	GTGTGTACAGGGTGTCCATTGCGCTGCAAGGCGCTCCGATACCACTCCACGGAGG	5712
QY	4573	AGTCTTACCATCACTCAGCTGTGAAGAGCTTCAACAGTGGATCAACAGGACTGCTCC	4632	Db	6301	GTGTGTACAGGGTGTCCATTGCGCTGCAAGGCGCTCCGATACCACTCCACGGAGG	6360
Db	5221	AGTCTTACCATCACTCAGCTGTGAAGAGCTTCAACAGTGGATCAACAGGACTGCTCC	5280	QY	5713	AAGAGACGGTGTCTCTGTACAGAACTACCGTGTCTTCTGCTTGGCGGAGTCCGCACA	5772
QY	4633	AGCCATGTCTCGGCTCTGGCTTAAGAGATGTTTGGGATTTGATATGACGGTGTGACT	4692	Db	6361	AAGAGACGGTGTCTCTGTACAGAACTACCGTGTCTTCTGCTTGGCGGAGTCCGCACA	6420
Db	5281	AGCCATGTCTCGGCTCTGGCTTAAGAGATGTTTGGGATTTGATATGACGGTGTGACT	5340	QY	5773	AAGACCTTCCGAGCTCCGAAATCGTCCGGCGTCCGATACCACTCCACGGAGG	5832
QY	4693	GAITTCAGACCTGGCTCCAGTCCAAAGCTCTCGCGGATTCGCGGAGTCCCTCTTTC	4752	Db	6421	AAGACCTTCCGAGCTCCGAAATCGTCCGGCGTCCGATACCACTCCACGGAGG	6480
Db	5341	GAITTCAGACCTGGCTCCAGTCCAAAGCTCTCGCGGATTCGCGGAGTCCCTCTTTC	5400	QY	5833	GACACGCTCCGACGACGCGGATCCGATCTCAGCGACGGGTCTTGGTCTACCGTAAGC	5892
QY	4753	TCATGTCAACGTTGGTACAGGGAGTCTGGCGGGGACGGCATCATGCAAAACACCTGC	4812	Db	6481	GACACGCTCCGACGACGCGGATCCGATCTCAGCGACGGGTCTTGGTCTACCGTAAGC	6540
Db	5401	TCATGTCAACGTTGGTACAGGGAGTCTGGCGGGGACGGCATCATGCAAAACACCTGC	5460	QY	5893	CCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAAGC	5952
QY	4813	CCATGTGGAGCAGATCACCGGACATGTGAAAGGTTCCATGAGGATCGTGGGGCT	4872	Db	6541	CCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAAGC	6600
Db	5461	CCATGTGGAGCAGATCACCGGACATGTGAAAGGTTCCATGAGGATCGTGGGGCT	5520	QY	5953	GAGAGGCTAGTGAAGAGCTGTCTGCTGCTGCTGCTTACATCATGACATGACATCTTTG	6012
QY	4873	AGGACCTGTAGTAAACGTTGGATGGAACATTTCCCAATTAACGGGTACACAGGGCCC	4932	Db	6601	GAGAGGCTAGTGAAGAGCTGTCTGCTGCTGCTTACATCATGACATGACATCTTTG	6660
Db	5521	AGGACCTGTAGTAAACGTTGGATGGAACATTTCCCAATTAACGGGTACACAGGGCCC	5580	QY	6013	ATCACGCCATGCGCTGGGAGGAAACCAAGCTGCCCCATCAATGCACTGAGCACTCTTG	6072
QY	4933	TGACGCCCTTCCCGGCCCAATTTATTTCTAGGCGCTGTGGCGGGTGGCTGTGAGAG	4992	Db	6661	ATCACGCCATGCGCTGGGAGGAAACCAAGCTGCCCCATCAATGCACTGAGCACTCTTG	6720
Db	5581	TGACGCCCTTCCCGGCCCAATTTATTTCTAGGCGCTGTGGCGGGTGGCTGTGAGAG	5640	QY	6073	CTCCGTCAACCAAACTTGGTCTATGTGTACAACTCTCGAGCGCAAGCTTGGCGAGAG	6132
QY	4993	TACGTGGAGGTACCGGGTGGGGATTTTCCATACGTGACGGGATGACCACTGACNAC	5052	Db	6721	CTCCGTCAACCAAACTTGGTCTATGTGTACAACTCTCGAGCGCAAGCTTGGCGAGAG	6780
Db	5641	TACGTGGAGGTACCGGGTGGGGATTTTCCATACGTGACGGGATGACCACTGACNAC	5700	QY	6133	AAGGTCACTTTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6192
QY	5053	GTAAAGTCCCGTGTGAGGTTCGGGCCCGCAATTTCTTCAAGAGTGGTGGGTGGG	5112	Db	6781	AAGGTCACTTTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6840
Db	5701	GTAAAGTCCCGTGTGAGGTTCGGGCCCGCAATTTCTTCAAGAGTGGTGGGTGGG	5760	QY	6193	ATGAAGGGGAGGGGCTCCACAGTTTAAAGGCTAAATTTCTATCCGTGGAGAGGCTGTGTA	6252
QY	5113	TTGCACAGGTACGCTCCAGCGTGCATAAACCCCTCTCTACGGGAGGAGGTCACTTCTGTGTC	5172				

Db 6841 ATGAAGGCGAAGCGGCTCCACAGTTAAGGCTAAACTTATCCGTCGAGGAAGCTGTAG 6900
QY 6253 CTGACGCCCCACATTTGGCCAGATCTAAATTTGGCTATGGGCAAGGACGTCGGGAC 6312
Db 6901 CTGACGCCCCACATTTGGCCAGATCTAAATTTGGCTATGGGCAAGGACGTCGGGAC 6960
QY 6313 CTATCAGCAAGCGGCTTAAACACATCCGCTCCGTCGTCGGAAGCACTTGTGGAAGACACT 6372
Db 6961 CTATCAGCAAGCGGCTTAAACACATCCGCTCCGTCGTCGGAAGCACTTGTGGAAGACACT 7020
QY 6373 GAGACACCAATTTGACACACACATCATGGCAAAAATAGGTTTTTCTGGTCCAAACAGAG 6432
Db 7021 GAGACACCAATTTGACACACACATCATGGCAAAAATAGGTTTTTCTGGTCCAAACAGAG 7080
QY 6433 AAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTTCCAGATTTGGGGGTTCTGTGTGC 6492
Db 7081 AAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTTCCAGATTTGGGGGTTCTGTGTGC 7140
QY 6493 GAGAAATGGCCCTTTACGATGGTCTCCACCTCCCTCAGGCCGTGATGGGCTCTTCA 6552
Db 7141 GAGAAATGGCCCTTTACGATGGTCTCCACCTCCCTCAGGCCGTGATGGGCTCTTCA 7200
QY 6553 TACGGATTTCCAAATCTCTCTGACAGCGGTCGAGTTCTCTGGTGAATGCTCGAAAGCG 6612
Db 7201 TACGGATTTCCAAATCTCTCTGACAGCGGTCGAGTTCTCTGGTGAATGCTCGAAAGCG 7260
QY 6613 AAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTGTGACTTGGCCCGGAGCCAGA 6732
Db 7261 AAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTGTGACTTGGCCCGGAGCCAGA 7380
QY 6673 AATGACATCCGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCGGAGCCAGA 6732
Db 7321 AATGACATCCGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCGGAGCCAGA 7380
QY 6733 CAGGCCATAAGTTCGCTCAGAGCGGCTTTACATCGGGGCCCTCTGACTAATCTAAA 6792
Db 7381 CAGGCCATAAGTTCGCTCAGAGCGGCTTTACATCGGGGCCCTCTGACTAATCTAAA 7440
QY 6793 GGGCAGAACTGCGGCTATCGCGGCTGCGCGAGCGGTGACTGAGCAGCAGCTGCGGT 6852
Db 7441 GGGCAGAACTGCGGCTATCGCGGCTGCGCGAGCGGTGACTGAGCAGCAGCTGCGGT 7500
QY 6853 AATACCTTCATGTTACTTTGAAGGCGCTGCGGCTGTCGAGTGCAGAGCTCCAGGAC 6912
Db 7501 AATACCTTCATGTTACTTTGAAGGCGCTGCGGCTGTCGAGTGCAGAGCTCCAGGAC 7560
QY 6913 TGCAAGATGCTCGTATGCGAGAGCGCTTGTGTTATCTGTGAAGCGCGGAGACCCAA 6972
Db 7561 TGCAAGATGCTCGTATGCGAGAGCGCTTGTGTTATCTGTGAAGCGCGGAGACCCAA 7620
QY 6973 GAGGACGAGGCGAGCTCAGGGCTTTACGAGGCTATGACTAGATACTCTGCCGCCCT 7032
Db 7621 GAGGACGAGGCGAGCTCAGGGCTTTACGAGGCTATGACTAGATACTCTGCCGCCCT 7680
QY 7033 GGGGACCCGCCAAACAGATACGCTTGGAGTGTGATTAACATCATGCTCTCCATGTG 7092
Db 7681 GGGGACCCGCCAAACAGATACGCTTGGAGTGTGATTAACATCATGCTCTCCATGTG 7740
QY 7093 TCAGTGGCGCAGATGCTATCTGCAAGAGGTTACTATCTACCGGTGACCCCAACC 7152
Db 7741 TCAGTGGCGCAGATGCTATCTGCAAGAGGTTACTATCTACCGGTGACCCCAACC 7800
QY 7153 CCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACCTCCAGTCAATTTCTGGCTAGGC 7212
Db 7801 CCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACCTCCAGTCAATTTCTGGCTAGGC 7860
QY 7213 AACATCATGATGTCGCCCACTTGTGGCAAGGATGATCTGATGACTCATTTCTTC 7272
Db 7861 AACATCATGATGTCGCCCACTTGTGGCAAGGATGATCTGATGACTCATTTCTTC 7920
QY 7273 TCCATCTTCTAGCTCAGGAACTTGAAGCCCTAGATTTGATGACTGACGAGGCGC 7332
Db 7921 TCCATCTTCTAGCTCAGGAACTTGAAGCCCTAGATTTGATGACTGACGAGGCGC 7980

QY 7333 TGTACTCCATGAGCCACTTGACCTACCTCAGATCATTCAACGACTCCATGSCCTTAGC 7392
Db 7981 TGTACTCCATGAGCCACTTGACCTACCTCAGATCATTCAACGACTCCATGSCCTTAGC 8040
QY 7393 GCATTTTCACTCCATAGTTACTCTCAGTGAGATCAATAGGTTGGCTTTCATGSCCTCAGG 7452
Db 8041 GCATTTTCACTCCATAGTTACTCTCAGTGAGATCAATAGGTTGGCTTTCATGSCCTCAGG 8100
QY 7453 AAACCTTGGGTTACGCGCTTGGAGTCTGGAGACATCGGCCAGAAAGTGTCCGCGCTAGG 7512
Db 8101 AAACCTTGGGTTACGCGCTTGGAGTCTGGAGACATCGGCCAGAAAGTGTCCGCGCTAGG 8160
QY 7513 CTACTGTCCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTCAACTGGGCACTA 7572
Db 8161 CTACTGTCCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTCAACTGGGCACTA 8220
QY 7573 AGGACCAAGCTCAAACTCAGCTCCCAATCCCGGCTGCTCCAGTTGGATTTATCCAGCTGG 7632
Db 8221 AGGACCAAGCTCAAACTCAGCTCCCAATCCCGGCTGCTCCAGTTGGATTTATCCAGCTGG 8280
QY 7633 TTCTGTGCTGGTTACAGCGGGGAGACATATATCAGAGCTGTCTCGTGCCGACCCCGC 7692
Db 8281 TTCTGTGCTGGTTACAGCGGGGAGACATATATCAGAGCTGTCTCGTGCCGACCCCGC 8340
QY 7693 TGGTTCATGTTGCTTACTCTACTTTCTGTAGGGGTAGGCATCTATCTACTCCCAAC 7752
Db 8341 TGGTTCATGTTGCTTACTCTACTTTCTGTAGGGGTAGGCATCTATCTACTCCCAAC 8400
QY 7753 CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTTTCCCTTTTT 7812
Db 8401 CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTTTCCCTTTTT 8460
QY 7813 TTTTCTTT 7872
Db 8461 TTTTCTTT 8520
QY 7873 TTTTCTTT 7932
Db 8521 TTTTCTTT 8580
QY 7933 GTCCGTGAGCCGCTTGAATGCTGAGAGTGTGATCTGAGCTCTCTGAGATCAAGT 7989
Db 8581 GTCCGTGAGCCGCTTGAATGCTGAGAGTGTGATCTGAGCTCTCTGAGATCAAGT 8637

Search completed: August 12, 2004, 09:38:29
Job time : 19781 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 02:12:50 ; Search time 1827 Seconds
(without alignments)
18583.251 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccccgcattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7985.6	99.9	7992	6	AAL47276 Hepatitis
2	7985.6	99.9	10690	6	Abk91412 Hepatitis
3	7985.6	99.9	10690	8	ACA61697 Hepatitis
4	7985.6	99.9	10690	9	ADC83762 Hepatitis
5	7984	99.9	7992	6	AAL47281 Hepatitis
6	7984	99.9	10690	6	Abk91448 Hepatitis
7	7984	99.9	10690	6	Abk91448 Hepatitis
8	7984	99.9	10690	6	Abk91435 Hepatitis
9	7984	99.9	10690	6	Abk91434 Hepatitis
10	7982.6	99.9	7989	3	Abk91443 Hepatitis
11	7982.4	99.9	10690	6	Abk91440 Hepatitis
12	7981	99.9	7989	6	AAL47280 Hepatitis
13	7980.8	99.9	7992	6	AAL47277 Hepatitis
14	7980.8	99.9	7992	6	AAL47277 Hepatitis
15	7980	99.8	7991	6	AAL47279 Hepatitis
16	7979.4	99.8	7989	6	AAL47279 Hepatitis
17	7977.6	99.8	10690	6	AAL47279 Hepatitis
18	7976.2	99.8	7989	6	AAL47279 Hepatitis
19	7976.2	99.8	7989	6	AAL47279 Hepatitis
20	7974.6	99.8	10691	6	AAL47279 Hepatitis
21	7972.6	99.8	10693	6	AAL47279 Hepatitis
22	7971	99.7	10693	6	AAL47279 Hepatitis
23	7969.8	99.7	10691	6	AAL47279 Hepatitis

ALIGNMENTS

RESULT 1

AAL47276

ID AAL47276 standard; DNA; 7992 BP.

XX

AC AAL47276;

XX

DT 30-AUG-2002 (first entry)

XX

DE Hepatitis C virus sub-genomic replicon clone I377-NS3-3'UTR.

XX

KW Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;

KW

KW virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX

OS Hepatitis C virus.

XX

Key Location/Qualifiers

FT CDS

342..1181

/*tag= a

FT CDS

/product= "core-neo fusion protein"

1801..7758

/*tag= b

FT CDS

/product= "NS3 proteinase/helicase"

XX

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XX

CC able to replicate efficiently when transfected into a susceptible cell
 CC line without reducing the growth rate of the cell line by more than 10
 CC fold. The sequences are useful for screening for anti-HCV therapeutics,
 CC for detecting antibodies to HCV in a biological sample such as blood,
 CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
 CC for deriving authentic HCV components such as replication-component, and replication-
 CC infectious, replication-defective infection-component, and replication-
 CC defective non-infectious HCV, in gene therapy or gene vaccination
 CC targeted to hepatic tissue for treating an animal infected or susceptible
 CC to HCV infection and for studying HCV infection and propagation. The
 CC present sequence is a clone of a fragment of the HCV genome which encodes
 CC the core-neo and NS3 proteinase/helicase proteins
 XX
 SQ Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;

Query Match 99.9%; Score 7985.6; DB 6; Length 7992;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 181 GACGACCCGGTCTTCTTGGATCAACCGCTCAATGCTGAGAGATTTGGGGTGGCCCC 240
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Db

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KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication.
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PA	
XX	
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DR	WPI; 2002-599793/64.
XX	
CC	New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT	NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT	ribosome entry site (IRES) region, useful in studying HCV replication and
PT	expression.
XX	
PS	Claim 1; Fig 1; 69pp; English.
XX	
CC	The invention relates to nucleic acid molecules comprising altered HCV
CC	NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC	internal ribosome entry site (IRES) region coding for one or more NS3,
CC	NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC	are detailed in the specification. Also included are (1) an expression
CC	vector comprising a nucleotide sequence coding for the altered nucleic
CC	acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC	recombinant cell human hepatoma cell comprising the altered nucleic acids
CC	; (3) a recombinant cell produced by introducing into a human hepatoma
CC	cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC	replicon enhanced cell or which containing a functional HCV replicon; (5)
CC	an HCV replicon enhanced cells made in the method; and (6) measuring the
CC	ability of a compound to affect HCV activity. The HCV replicons and HCV
CC	replicon enhanced cells are useful in studying HCV replication and
CC	expression, and HCV and host cell interactions, producing HCV RNA and
CC	proteins, and providing a system for measuring the ability of a compound
CC	to modulate one or more HCV activities e.g. to discover drugs which may
CC	treat HCV mediated diseases such as liver failure, cirrhosis and
CC	hepatocellular carcinoma. The present sequence is the HCV based vector
CC	pHCVNeo.17, used as a basis for the adaptive mutations of the invention
XX	
SQ	Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
	Query Match 99.9%; Score 7985.6; DB 6; Length 10690;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0
QY	1 GCCAGCCCCGATGTGGGGCGACATCTCACCATAGATCACTCCCCTGTGAGGAAGTACTG 60
DB	1 GCCAGCCCCGATGTGGGGCGACATCTCACCATAGATCACTCCCCTGTGAGGAAGTACTG 60
QY	61 TCTTCACGCAGAAGCGTCTTAGCCATGGCGTTAGTGATGTCGTGACGCTCCAGGAC 120
DB	61 TCTTCACGCAGAAGCGTCTTAGCCATGGCGTTAGTGATGTCGTGACGCTCCAGGAC 120
QY	121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACGGGTGAGTACACCGGAATTGCCAG 180
DB	121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACGGGTGAGTACACCGGAATTGCCAG 180
QY	181 GACGACC GG GT C TT TT TG AT GA CA ACC CG CT CA TC CC TT GG AG ATT TGG CG CT GC CC CC 240

Db	1261	CGAAGCCGCTTTGGAAATAAGGCGGCTGTGCGTTTGTCTATATGTTATTTTCCACCATATTG	1321
Qy	1321	CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT	1380
Db	1321	CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT	1380
Qy	1381	AGGGGTCTTTTCCCTCTCCCAAGGAATGCAAGGTCTGTTGAAATGCTCTGGAAGGAACA	1440
Db	1381	AGGGGTCTTTTCCCTCTCCCAAGGAATGCAAGGTCTGTTGAAATGCTCTGGAAGGAACA	1440
Qy	1441	GTTCCTCTGGAAGCTTCTTGAAACAACAACAGTCTGTAGCGACCCCTTTGCAGGCAGCG	1500
Db	1441	GTTCCTCTGGAAGCTTCTTGAAACAACAACAGTCTGTAGCGACCCCTTTGCAGGCAGCG	1500
Qy	1501	AACCCCCACCTGGCGACAGGTGCTCTGCGGCCAAAGACCAACGCTGTATAAGATACACT	1560
Db	1501	AACCCCCACCTGGCGACAGGTGCTCTGCGGCCAAAGACCAACGCTGTATAAGATACACT	1560
Qy	1561	GCAAAGGGGCACAACCCACAGTGCCACGTGTGAGTTGGATAGTTGTGGAAGAGTCAAA	1620
Db	1561	GCAAAGGGGCACAACCCACAGTGCCACGTGTGAGTTGGATAGTTGTGGAAGAGTCAAA	1620
Qy	1621	TGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCGCAAGAGTACCCCATTTGT	1680
Db	1621	TGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCGCAAGAGTACCCCATTTGT	1680
Qy	1681	ATGGGATCTGATCTGGGGCCCTCGGTGCACATGCTTTACATGTTTGTAGTTCAGGTTAAAA	1740
Db	1681	ATGGGATCTGATCTGGGGCCCTCGGTGCACATGCTTTACATGTTTGTAGTTCAGGTTAAAA	1740
Qy	1741	AAGCTTAGGCCCCCGAAACAAGGGACGTGGTTCCTTTGAAAAACGATAATACC	1800
Db	1741	AAGCTTAGGCCCCCGAAACAAGGGACGTGGTTCCTTTGAAAAACGATAATACC	1800
Qy	1801	ATGGCGCTATTACGCGCTACTCCCAACAGCGAGGCTTACTTGGCTGCATCATCACT	1860
Db	1801	ATGGCGCTATTACGCGCTACTCCCAACAGCGAGGCTTACTTGGCTGCATCATCACT	1860
Qy	1861	AGCTCACAGGCGCGGACAGGAACCAAGTTCAGGGGAGGTCGCAAGTGGTCTCCACCGCA	1920
Db	1861	AGCTCACAGGCGCGGACAGGAACCAAGTTCAGGGGAGGTCGCAAGTGGTCTCCACCGCA	1920
Qy	1921	ACACATCTTCTTGGGACCTCGCTCAATGGCGTGTGTTGGAATGCTATCATGTTGCC	1980
Db	1921	ACACATCTTCTTGGGACCTCGCTCAATGGCGTGTGTTGGAATGCTATCATGTTGCC	1980
Qy	1981	GGCTCAAGACCTTCCCGGCCCAAGGGCCCAATCACCAGATGACCAATGTGGAC	2040
Db	1981	GGCTCAAGACCTTCCCGGCCCAAGGGCCCAATCACCAGATGACCAATGTGGAC	2040
Qy	2041	CAGGACCTCGTCGGCTGGCAAGCGCCCCCGGGCGCTTCTTTGACACCATGCACCTGC	2100
Db	2041	CAGGACCTCGTCGGCTGGCAAGCGCCCCCGGGCGCTTCTTTGACACCATGCACCTGC	2100
Qy	2101	GGGAGCTCGGACCTTACTTGTGTACAGAGCATGCCGATGTCAATCCGGTGCGCCGCGG	2160
Db	2101	GGGAGCTCGGACCTTACTTGTGTACAGAGCATGCCGATGTCAATCCGGTGCGCCGCGG	2160
Qy	2161	GGGACACAGGGGGAGCTACTCTCCCCAGGCGGCTCTTCTTGGAGGGCTCTTCG	2220
Db	2161	GGGACACAGGGGGAGCTACTCTCCCCAGGCGGCTCTTCTTGGAGGGCTCTTCG	2220
Qy	2221	GGGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCTCTTTTCGGGCTGCCGTTGC	2280
Db	2221	GGGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCTCTTTTCGGGCTGCCGTTGC	2280
Qy	2281	ACCGAGGGGTGGAAGGGCGGTGGACTTTGTACCGTTCAGTCTATGGAACCATATG	2340
Db	2281	ACCGAGGGGTGGAAGGGCGGTGGACTTTGTACCGTTCAGTCTATGGAACCATATG	2340
Qy	2341	CGGTCCCCGGTCTTTCACGGACAACCTGCTCCCTCCGGCCGTCACCGAGACATTCAGGTG	2400
Db	2341	CGGTCCCCGGTCTTTCACGGACAACCTGCTCCCTCCGGCCGTCACCGAGACATTCAGGTG	2400

QY	2401	GC	CCATCTACAGCC	CCCTACTG	TAGCGCAAGAC	TAAAGTGC	CGCTCGTATGCA	2461	
DB	2401	GC	CCATCTACAGCC	CCCTACTG	TAGCGCAAGAC	TAAAGTGC	CGCTCGTATGCA	2460	
QY	2461	GC	CCAAAGG	TATAGG	TCCTGTCT	GAAACCGTCCG	TCCGCGCACCC	2520	
DB	2461	GC	CCAAAGG	TATAGG	TCCTGTCT	GAAACCGTCCG	TCCGCGCACCC	2520	
QY	2521	GC	GTATATGTCT	TAAGGCACAT	GGTATCGAC	CCTTAACATCAG	AACCGGGTAAGGACCATC	2580	
DB	2521	GC	GTATATGTCT	TAAGGCACAT	GGTATCGAC	CCTTAACATCAG	AACCGGGTAAGGACCATC	2580	
QY	2581	AC	CAGGGTCC	CCCATC	ACGTACTCC	ACCTATGGCAAG	TTCTTTGCCGACGGTGTGC	2640	
DB	2581	AC	CAGGGTCC	CCCATC	ACGTACTCC	ACCTATGGCAAG	TTCTTTGCCGACGGTGTGC	2640	
QY	2641	TC	TGGGGCGC	CTATG	ATCATATAT	TGTGATGAG	TGCCCATCAACTGACTCGACCAT	2700	
DB	2641	TC	TGGGGCGC	CTATG	ATCATATAT	TGTGATGAG	TGCCCATCAACTGACTCGACCAT	2700	
QY	2701	AT	CTTG	GGCATCGG	CACTCTG	GCACCAAG	CGAGCGCTGAGCGCGGACTCGTCGTG	2760	
DB	2701	AT	CTTG	GGCATCGG	CACTCTG	GCACCAAG	CGAGCGCGCTGAGCGCGGACTCGTCGTG	2760	
QY	2761	CT	CGCCAC	CGCTAC	CGCTCCGG	ATCGGTCA	CCGTGCCACATCCAAATCGAGGAGGTG	2820	
DB	2761	CT	CGCCAC	CGCTAC	CGCTCCGG	ATCGGTCA	CCGTGCCACATCCAAATCGAGGAGGTG	2820	
QY	2821	GC	CTCTCCAG	CACTGG	AGAAATCC	CCCTTTATGG	CAAAAGCCAPCCCATCGAGACCATC	2880	
DB	2821	GC	CTCTCCAG	CACTGG	AGAAATCC	CCCTTTATGG	CAAAAGCCAPCCCATCGAGACCATC	2880	
QY	2881	AA	GGGGG	GAGG	CACTCAT	TTTCTGC	CAATCCAAAGAAATGTGATGAGCTCGCGCG	2940	
DB	2881	AA	GGGGG	GAGG	CACTCAT	TTTCTGC	CAATCCAAAGAAATGTGATGAGCTCGCGCG	2940	
QY	2941	AA	GTCTCG	GGCTCG	GCATCA	ATGTGTAG	CAATATTACCGGGCCCTTGATGATCCGTC	3000	
DB	2941	AA	GTCTCG	GGCTCG	GCATCA	ATGTGTAG	CAATATTACCGGGCCCTTGATGATCCGTC	3000	
QY	3001	AT	ACCAACT	AGCGG	ACGTCTAT	TGCTAG	CAAGCGAC	CGCTCTAATGACGGGCTTTACC	3060
DB	3001	AT	ACCAACT	AGCGG	ACGTCTAT	TGCTAG	CAAGCGAC	CGCTCTAATGACGGGCTTTACC	3060
QY	3061	GG	CGATTT	CGACT	CGATGAT	CGACT	CGAATACATG	TGTACCCAGACAGT	3120
DB	3061	GG	CGATTT	CGACT	CGATGAT	CGACT	CGAATACATG	TGTACCCAGACAGT	3120
QY	3121	CT	GGAAC	CGCACTT	CAACAT	TGAG	CGACCGCTGCCAAG	ACGGGTGTCA	3180
DB	3121	CT	GGAAC	CGCACTT	CAACAT	TGAG	CGACCGCTGCCAAG	ACGGGTGTCA	3180
QY	3181	CAG	CGCGG	CAG	CAGCTGT	AGGGC	AGGATG	GGCATTTACAGTTTGTGACTCCAGGA	3240
DB	3181	CAG	CGCGG	CAG	CAGCTGT	AGGGC	AGGATG	GGCATTTACAGTTTGTGACTCCAGGA	3240
QY	3241	GA	ACGGCC	CTCGG	CAATGTT	CGATTCC	TCTCGGTTC	TGTGCGAGTGTATGACCGGGCTGT	3300
DB	3241	GA	ACGGCC	CTCGG	CAATGTT	CGATTCC	TCTCGGTTC	TGTGCGAGTGTATGACCGGGCTGT	3300
QY	3301	GCT	TGGTAC	GAGCTCA	CGCCCG	CGAGACCT	CAGTTAG	GTTCGGGCTTTACCTAAACACA	3360
DB	3301	GCT	TGGTAC	GAGCTCA	CGCCCG	CGAGACCT	CAGTTAG	GTTCGGGCTTTACCTAAACACA	3360
QY	3361	CC	AGGTTGCC	CGTCTG	CCAGAC	CAATCTG	GAGTTCTGG	GAGCGTCTTTACAGSCCTC	3420
DB	3361	CC	AGGTTGCC	CGTCTG	CCAGAC	CAATCTG	GAGTTCTGG	GAGCGTCTTTACAGSCCTC	3420
QY	3421	AC	CCACATAG	ACGCC	ATTTCTTGT	CCAGACTA	AGCAGG	CAGGACAACTTCCCTAC	3480
DB	3421	AC	CCACATAG	ACGCC	ATTTCTTGT	CCAGACTA	AGCAGG	CAGGACAACTTCCCTAC	3480

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Qy	3481	CTGGTAGCATACAGGCTAGGTTGTCGGCCAGGCTCAGGCTCCACCTCCATCGTGGGAC	3540	Db	4561	CAGATCCTCTCTAGTCTTTACCATCACTCAGCTGCTGAGAGGCTTCACCGATGGATCAAC	4620
Db	3481	CTGGTAGCATACAGGCTAGGTTGTCGGCCAGGCTCAGGCTCCACCTCCATCGTGGGAC	3540	Qy	4621	GAGACTGCTCCACGCCATGCTCCGGCTCCTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680
Qy	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGGCTTACGCTGCACGGGCAACGGCCCTGCTG	3600	Db	4621	GAGACTGCTCCACGCCATGCTCCGGCTCCTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680
Db	3541	CAAAATGTGGAAGTGTCTCATACGGCTTAAAGCTTACGCTGCACGGGCAACGGCCCTGCTG	3600	Qy	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGGCCGCGATTTGCCGGGA	4740
Qy	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACACCCCAATACCAATACATC	3660	Db	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGGCCGCGATTTGCCGGGA	4740
Db	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACACCCCAATACCAATACATC	3660	Qy	4741	GTCCCTCTTCTTCATGTCAACGTGGGTACAAAGGGAGTCTGGCGGGCGACGGCATCATG	4800
Qy	3661	ATGGCATGCAATGTCGGCTGACCTGGAGTTCGTCACGAGCACCTGGGTGCTGGTAGGCGGA	3720	Db	4741	GTCCCTCTTCTTCATGTCAACGTGGGTACAAAGGGAGTCTGGCGGGCGACGGCATCATG	4800
Db	3661	ATGGCATGCAATGTCGGCTGACCTGGAGTTCGTCACGAGCACCTGGGTGCTGGTAGGCGGA	3720	Qy	4801	CAAAACCACTGCCTTTCATGTGAGAGCACAGATCAACGGGACATGTGAAAAAAGTTTCCATGAGG	4860
Qy	3721	GTCTTAGCAGCTCTGGCGCGGTAATTGCTTGACAAACAGGCAAGCGTGTCAATTGTGGGAGG	3780	Db	4801	CAAAACCACTGCCTTTCATGTGAGAGCACAGATCAACGGGACATGTGAAAAAAGTTTCCATGAGG	4860
Db	3721	GTCTTAGCAGCTCTGGCGCGGTAATTGCTTGACAAACAGGCAAGCGTGTCAATTGTGGGAGG	3780	Qy	4861	ATCGTGGGGCTTAGACACCTGTAGTAACACGTGGCATGGAACAATTTCCATTAACCGCGTAC	4920
Qy	3781	ATCATCTTGTCCGGAAGCCCGGCCATCATTTCCCGACAGGGAAGTTCCTTTACCGGGAGTTTC	3840	Db	4861	ATCGTGGGGCTTAGACACCTGTAGTAACACGTGGCATGGAACAATTTCCATTAACCGCGTAC	4920
Db	3781	ATCATCTTGTCCGGAAGCCCGGCCATCATTTCCCGACAGGGAAGTTCCTTTACCGGGAGTTTC	3840	Qy	4921	ACCAAGGGCCCTGCACGCCCTCCCGGGCGCAAAATTAATTCAGGGCGCTGTGGCGGGTG	4980
Qy	3841	GATGAGTAGGAGAGTGGCTCACCTCCCTTACATTCGAAACAGGGAATGCAGCTCGCC	3900	Db	4921	ACCAAGGGCCCTGCACGCCCTCCCGGGCGCAAAATTAATTCAGGGCGCTGTGGCGGGTG	4980
Db	3841	GATGAGTAGGAGAGTGGCTCACCTCCCTTACATTCGAAACAGGGAATGCAGCTCGCC	3900	Qy	4981	GCTGCTAGGAGTAGCTGAGGTTTACGGCGGTGGGGATTTTCCACTAGCTGACGGGCGATG	5040
Qy	3901	GAACAATTTCAACAGAGGCAATCGGTTGTGCAACACAGCCACCAAGACGAGGAGGCT	3960	Db	4981	GCTGCTAGGAGTAGCTGAGGTTTACGGCGGTGGGGATTTTCCACTAGCTGACGGGCGATG	5040
Db	3901	GAACAATTTCAACAGAGGCAATCGGTTGTGCAACACAGCCACCAAGACGAGGAGGCT	3960	Qy	5041	ACCACTGACAAACGTAAAGTGCCTGTACAGTTCCGGCCCCCGAAATTTCTTCACAGAAGTG	5100
Qy	3961	GCTGCTCCCGTGGTGGAAATCCMAAGTGGCGGACCTTCGAGAGCTTGTCCACTCTGCCCTGCAACCCC	4020	Db	5041	ACCACTGACAAACGTAAAGTGCCTGTACAGTTCCGGCCCCCGAAATTTCTTCACAGAAGTG	5100
Db	3961	GCTGCTCCCGTGGTGGAAATCCMAAGTGGCGGACCTTCGAGAGCTTGTCCACTCTGCCCTGCAACCCC	4020	Qy	5101	GATGGGTTGGGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGAGTCT	5160
Qy	4021	TGGAAATTTCAACAGAGGCAATCGGTTGTGCAACACAGCCACCAAGACGAGGAGGCT	4080	Db	5101	GATGGGTTGGGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGAGTCT	5160
Db	4021	TGGAAATTTCAACAGAGGCAATCGGTTGTGCAACACAGCCACCAAGACGAGGAGGCT	4080	Qy	5161	ACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATTCGGAGCCCCGAA	5220
Qy	4081	GGGATAGCATCACTGATGSCATTTACAGCCTCTATCACAGCCCGCTCACCAACCCCAAT	4140	Db	5161	ACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATTCGGAGCCCCGAA	5220
Db	4081	GGGATAGCATCACTGATGSCATTTACAGCCTCTATCACAGCCCGCTCACCAACCCCAAT	4140	Qy	5221	CCGGAAGTAGAGTGTCTCACTTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGACG	5280
Qy	4141	ACCTCTCTTTTAAACATCTCGGGGGATGGGTGGCGCCCACTTGTCTCTCCACAGCGCT	4200	Db	5221	CCGGAAGTAGAGTGTCTCACTTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGACG	5280
Db	4141	ACCTCTCTTTTAAACATCTCGGGGGATGGGTGGCGCCCACTTGTCTCTCCACAGCGCT	4200	Qy	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTGTTGGCGAGTATCAGCTACGCCAG	5340
Qy	4201	GCTTCGCTTTTCTAGCGCGCGGATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTGTTGGCGAGTATCAGCTACGCCAG	5340
Db	4201	GCTTCGCTTTTCTAGCGCGCGGATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTTGGG	4260	Qy	5341	CTGTCGCGCTTCTTGAAGGCAACATGCATCTACCGCTCATCAGCTCCCGGACGCTGAC	5400
Qy	4261	AAGGTGCTGTGGAAATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCTCTGGGC	4320	Db	5341	CTGTCGCGCTTCTTGAAGGCAACATGCATCTACCGCTCATCAGCTCCCGGACGCTGAC	5400
Db	4261	AAGGTGCTGTGGAAATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCTCTGGGC	4320	Qy	5401	CTCATTCAGGCAACCTCTCTGTGGCGCAGGAGTGGCGGGGAACAACAACCCGCTGGAG	5460
Qy	4321	TTTAAAGTCATAGCGCGGAGATGCTCCACCGAGGACCTGGTAAACCTACTCCCTGCT	4380	Db	5401	CTCATTCAGGCAACCTCTCTGTGGCGCAGGAGTGGCGGGGAACAACAACCCGCTGGAG	5460
Db	4321	TTTAAAGTCATAGCGCGGAGATGCTCCACCGAGGACCTGGTAAACCTACTCCCTGCT	4380	Qy	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTGAGCCGCTCCAAGCGGAGGAGTATGAG	5520
Qy	4381	ATCCTCTCCCTCGGCGCTTAGTCTGTCGGGTCGTCGCGAGGATATCTGCTCGGCAC	4440	Db	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTGAGCCGCTCCAAGCGGAGGAGTATGAG	5520
Db	4381	ATCCTCTCCCTCGGCGCTTAGTCTGTCGGGTCGTCGCGAGGATATCTGCTCGGCAC	4440	Qy	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTTCGGAGGTTCCAGGAAATTTCCCTTCGAGCGATG	5580
Qy	4441	GTGGGCCACGAGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGGTTTCG					

	7861	TTTTCTCCTCTTTTTTCCTTTCTCCATCTTGCGGCTGCCATCTTAGCCCCTAGTCAACGGC	7920
Db	7861	TTTTTCTCCTTTTTTTTCCTTTCTCCATCTTGCGGCTGCCATCTTAGCCCCTAGTCAACGGC	7920
Qy	7921	TAGCTGTGAAGGTCCTGTAGCCGCCTTTACTGTCAGAGAGTGTGATACTGGCCCTCTTCG	7980
Db	7921	TAGCTGTGAAGGTCCTGTAGCCGCCTTTACTGTCAGAGAGTGTGATACTGGCCCTCTTCG	7980
Qy	7981	AGATCAAAGTA CT 7992 	
Db	7981	AGATCAAAGTA CT 7992 	
<hr/>			
	RESULT 3		
	ACA61697 standard; DNA; 10690 BP.		
XX	ACA61697;		
XX	11-AUG-2003 (first entry)		
DT	Hepatitis C virus expression plasmid pHCVneo17.wt DNA.		
DE	Hepatitis C virus; ds; gene; thiosemicarbazone; liver inflammation;		
XX	KW liver failure; cirrhosis.		
KW	XO Hepatitis C virus.		
OS	Synthetic.		
XX			
FH	Key Location/Qualifiers		
FT	1..341		
FT	/tag= "a"		
FT	/note= "HCV 5'UTR"		
FT	342..1181		
FT	/tag= b		
FT	/note= "Core-neo fusion protein selectable marker"		
FT	1190..1800		
FT	/tag= c		
FT	/note= "Internal ribosome entry site of encephalomyocarditis virus"		
FT	1801..7758		
CDS	/tag= d		
FT	/note= "HCV polyprotein coding sequence"		
FT	mat_peptide		
FT	1801..3696		
FT	/tag= e		
FT	/note= "Non-structural protein 3"		
FT	3697..3858		
FT	/tag= f		
FT	/note= "Non-structural protein 4A"		
FT	3859..4641		
FT	/tag= g		
FT	/note= "Non-structural protein 4B"		
FT	4642..5982		
FT	/tag= h		
FT	/note= "Non-structural protein 5A"		
FT	5983..7755		
FT	/tag= i		
FT	/note= "Non-structural protein 5B and RNA-dependent RNA polymerase"		
FT	7759..7989		
FT	/tag= j		
FT	/note= "HCV 3'UTR"		
XX			
PN	US2003045568-A1.		
XX			
PD	06-MAR-2003 .		
XX			
PF	19-APR-2002; 2002US-00125940.		
XX			
PR	20-APR-2001; 2001US-0285104P.		
XX	(ALTA/) ALTAMURA S. (KOCH/) KOCH U.		
PA			
PA			

XX	Altamura S, Koch U;
PI	XX
XX	WPI; 2003-447715/42.
DR	XX
XX	Treating infections by hepatitis C virus and its related conditions
PT	comprises administering thiosemicarbazone compounds.
FT	
XX	Example 2; Page 9-14; 25pp; English.
PS	XX
XX	The invention relates to a method of treating or preventing infection by
CC	hepatitis C virus or its related conditions by delaying the onset and
CC	inhibiting replication of hepatitis C virus which comprises administering
CC	thiosemicarbazone compounds. The method is useful for treating or
CC	preventing infection by hepatitis C virus or its related conditions e.g.
CC	liver inflammation, liver failure or cirrhosis, delaying the onset and
CC	inhibiting replication of hepatitis C. The present sequence represents
CC	the hepatitis C virus expression plasmid pHCVNeo17.wt DNA
XX	Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
XX	
SQ	
	Query Match 99.9%; Score 7985.6; DB 8; Length 10690;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy	1 GCCAGCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACTA CTG 60
Dd	
	1 GCCAGCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACTA CTG 60
Oy	61 TC TTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTAGTGTCGTGCAGCCTCAGGAC 120
Dd	
	61 TC TTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTAGTGTCGTGCAGCCTCAGGAC 120
Oy	121 CCCCCCTCCGGGAGAGCCATAGTGTCGCGAACCGGTGAGTACACGGGAATGCCAG 180
Dd	
	121 CCCCCCTCCGGGAGAGCCATAGTGTCGCGAACCGGTGAGTACACGGGAATGCCAG 180
Oy	181 GACGACCGGTCCTTTCTTGGATCAACCCCGCTCAATGCTGGAGATTTGGGCGTGCCCC 240
Dd	
	181 GACGACCGGTCCTTTCTTGGATCAACCCCGCTCAATGCTGGAGATTTGGGCGTGCCCC 240
Oy	241 GCGAGACTGCTAGCCGAGTAGTGTTGGGTGCGAAAAGCGTTGTGGTACTGCTCATFAGG 300
Dd	
	241 GCGAGACTGCTAGCCGAGTAGTGTTGGGTGCGAAAAGCGCTTGTGGTACTGCTCATFAGG 300
Oy	301 GTGCTTGGAGTGGCCCCGGGAGGTCGTAGACCGTGCACCATGAGCAGAATCCTA AAC 360
Dd	
	301 GTGCTTGGAGTGGCCCCGGGAGGTCGTAGACCGTGCACCATGAGCAGAATCCTA AAC 360
Oy	361 CTC AAGAAAAACCAAAGGCGCGCATGATTGAACAAGATGGATTGCA CGCAGGTTCTC 420
Dd	
	361 CTC AAGAAAAACCAAAGGCGCGCATGATTGAACAAGATGGATTGCA CGCAGGTTCTC 420
Oy	421 CGGCGCTTTGGGTGGAGAGGCTATTGGCTATGACTTGGGCA CAACAGCAATCGGCTGCT 480
Dd	
	421 CGGCGCTTTGGGTGGAGAGGCTATTGGCTATGACTTGGGCA CAACAGCAATCGGCTGCT 480
Oy	481 CTGATGCCCGCGHTTCCGCTGTGAGCGAGGGCGCCGGTTCCTTTTGTCAAGACCG 540
Dd	
	481 CTGATGCCCGCGHTTCCGCTGTGAGCGAGGGCGCCGGTTCCTTTTGTCAAGACCG 540
Oy	541 ACCGTGTCGCGTGCCTGAATGAAC TGACGAGCGAGGCGCGGCTATCGTGCTGGCCA 600
Dd	
	541 ACCGTGTCGCGTGCCTGAATGAAC TGACGAGCGAGGCGCGGCTATCGTGCTGGCCA 600
Oy	601 CGACGGGCGGTTCTTCGCGAGCTGTGCTCGA COTTGTCTACTGAAGCGGGAAGGACTGGC 660
Dd	
	601 CGACGGGCGGTTCTTCGCGAGCTGTGCTCGA COTTGTCTACTGAAGCGGGAAGGACTGGC 660
Oy	661 TGCTATTGGCGAAGTGCCGGGCGAGATCTCCTGT CATCTCACCTTGTCTCTCGCCGAGA 720
Dd	
	661 TGCTATTGGCGAAGTGCCGGGCGAGATCTCCTGT CATCTCACCTTGTCTCTCGCCGAGA 720

QY	721	AAATATCCATCATGGCTGTATGCAATGCGCGCTGTCATACGCTTCATCCGGCTACCTGCC	780
Db	721	AAATATCCATCATGGCTGTATGCAATGCGCGCTGTCATACGCTTCATCCGGCTACCTGCC	780
QY	781	CAATTGACCACCAAGCGAAATCGCATCGACGAGCAGCTACTCGGATGGAAGCCGGTC	840
Db	781	CAATTGACCACCAAGCGAAATCGCATCGACGAGCAGCTACTCGGATGGAAGCCGGTC	840
QY	841	TTGTTCGATCAGGATGATCTTGGACGAAGAGCATCAGGGCTCGCGCAGCGAATGTTTCG	900
Db	841	TTGTTCGATCAGGATGATCTTGGACGAAGAGCATCAGGGCTCGCGCAGCGAATGTTTCG	900
QY	901	CCAGGCTCAAGCGCGCATGCGCCGACGAGATCTCGTGTGACCATCGCGATGCCT	960
Db	901	CCAGGCTCAAGCGCGCATGCGCCGACGAGATCTCGTGTGACCATCGCGATGCCT	960
QY	961	GCTTCCCGAATCATGTTGGAAATGCGCGCTTTTCTGGATTTCAATCGACTGTGCCCGC	1020
Db	961	GCTTCCCGAATCATGTTGGAAATGCGCGCTTTTCTGGATTTCAATCGACTGTGCCCGC	1020
QY	1021	TGGGTGTGCGGACCGCTACTCAGGACATAGCGTTGGCTACCCGCTGATATTCCTGAAGC	1080
Db	1021	TGGGTGTGCGGACCGCTACTCAGGACATAGCGTTGGCTACCCGCTGATATTCCTGAAGC	1080
QY	1081	TTGGCGCGGAATGGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTCGC	1140
Db	1081	TTGGCGCGGAATGGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTCGC	1140
QY	1141	AGCGCATCGCCTTCTATCGCCTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACG	1200
Db	1141	AGCGCATCGCCTTCTATCGCCTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACG	1200
QY	1201	GTTTCCCTCTAGCGGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGC	1260
Db	1201	GTTTCCCTCTAGCGGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGC	1260
QY	1261	CGAAGCGCTTGGAAATGAAGCGGTGTGGTTGTCTATATGTTATTTTCCACATATTG	1320
Db	1261	CGAAGCGCTTGGAAATGAAGCGGTGTGGTTGTCTATATGTTATTTTCCACCAATTG	1320
QY	1321	CCGTCTTTTGGCAATGTAGGGCCCGGAACCTGGCCCTCTCTTTGACGAGCATTCCT	1380
Db	1321	CCGTCTTTTGGCAATGTAGGGCCCGGAACCTGGCCCTCTCTTTGACGAGCATTCCT	1380
QY	1381	AGGGGTCCTTCCCTCTCGCCAAAGGAATGCAAGGTCCTGTTGAATCTGCTGAGGAGCA	1440
Db	1381	AGGGGTCCTTCCCTCTCGCCAAAGGAATGCAAGGTCCTGTTGAATCTGCTGAGGAGCA	1440
QY	1441	GTTTCTCTGGAAGTCTTGAAGACAAACAACTGCTGTAGCGACCTTTGACGGCAGCG	1500
Db	1441	GTTTCTCTGGAAGTCTTGAAGACAAACAACTGCTGTAGCGACCTTTGACGGCAGCG	1500
QY	1501	AAACCCCACTCGGACAGTGCCTTCGGGCCAAAGCCACGTCGTATAAGATACCT	1560
Db	1501	AAACCCCACTCGGACAGTGCCTTCGGGCCAAAGCCACGTCGTATAAGATACCT	1560
QY	1561	GCAAGCGGCACAACCCCACTGTCAGTTGGATGAGTTGCTGGAAGAGTCAAA	1620
Db	1561	GCAAGCGGCACAACCCCACTGTCAGTTGGATGAGTTGCTGGAAGAGTCAAA	1620
QY	1621	TGGCTCTCTCAAGCGTATTCAAGAGGGGCTGAAGGATGCCCAGAAGTACCCCATTTG	1680
Db	1621	TGGCTCTCTCAAGCGTATTCAAGAGGGGCTGAAGGATGCCCAGAAGTACCCCATTTG	1680
QY	1681	ATGGGATCTGATCTGGGGCTCGGTSCATGCTTTACATGTTGTTTGTGAGGTTTAAA	1740
Db	1681	ATGGGATCTGATCTGGGGCTCGGTSCATGCTTTACATGTTGTTTGTGAGGTTTAAA	1740
QY	1741	ACGCTTAGCGCCCGGAAACACCGGGGAGCTGGTTTCTTTGAAAAACAGATAATCC	1800
Db	1741	ACGCTTAGCGCCCGGAAACACCGGGGAGCTGGTTTCTTTGAAAAACAGATAATCC	1800
QY	1801	ATGGCGCCTTATACGCGCTACTCCCAACAGACGAGCGGCGCTACTTGGCTGATCATCACT	1860

Db	1801	ATGGCGCCTATTATACGGCCCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT	186
Qy	1851	AGCCTCACAGGCGGGGACAGGAACACAGGTCAGAGGGGAGGTCCAGTGGTCTCCACCGCA	1920
Db	1861	AGCCTCACAGGCGGGGACAGGAACAGGTCGAGGGGGAGGTCCAAGTGGTCTCCACCGCA	1920
Qy	1921	ACACAATCTTCTTG6G6GACCTGCGTCAATGGCGTGTGTTGGACGTCTATCATGTGTC	1980
Db	1921	ACACAATCTTCTTG6G6GACCTGCGTCAATGGCGTGTGTTGGACGTCTATCATGTGTC	1980
Qy	1981	GGCTCAAAGACCTTTGCGGCGCCAAAGAGGCCCAATCACCCAATGTACACCAATGTGGAC	2040
Db	1981	GGCTCAAAGACCTTTGCGGCGCCAAAGAGGCCCAATCACCCAATGTACACCAATGTGGAC	2040
Qy	2041	CAGACCTCGTTCGGCTGGCAAGCGCCCCCGGGGCGCTTCCTTGACACCATGTGCACCTGC	2100
Db	2041	CAGACCTCGTTCGGCTGGCAAGCGCCCCCGGGGCGCTTCCTTGACACCATGTGCACCTGC	2100
Qy	2101	GGCAGCTTCGACCTTTACTTGGTCAGAGGCGATGCGATGTCATTCGGTGC CGCGCGG	2160
Db	2101	GGCAGCTTCGACCTTTACTTGGTCAGAGGCGATGCGATGTCATTCGGTGC CGCGCGG	2160
Qy	2161	GGCGACAGCAGGGGAGCCTACTCTCCGCCAGGCCGCTCCCTACTTGAAGGCTCTTCG	2220
Db	2161	GGCGACAGCAGGGGAGCCTACTCTCCGCCAGGCCGCTCCCTACTTGAAGGCTCTTCG	2220
Qy	2221	GGCGGTCCAATGCTCTGCCCTCGGGGACGCTGTGGGCATCTTTCGGGCTGCCGTGTC	2280
Db	2221	GGCGGTCCAATGCTCTGCCCTCGGGGACGCTGTGGGCATCTTTCGGGCTGCCGTGTC	2280
Qy	2281	ACCCGAGGGTTCGGAAGGCGGTGGACTTTGTACCCCGTCCAGTCTATGGAACCACTATG	2340
Db	2281	ACCCGAGGGTTCGGAAGGCGGTGGACTTTGTACCCCGTCCAGTCTATGGAACCACTATG	2340
Qy	2341	CGGTCCCCGTCTTCAAGCAACAACCTCGTCCCTTCGGGCCGTAACGAGACATTCAGGTG	2400
Db	2341	CGGTCCCCGTCTTCAAGCAACAACCTCGTCCCTTCGGGCCGTAACGAGACATTCAGGTG	2400
Qy	2401	GGCCATCTACAGCCCCCTACTGTTAGGGGACAGGACTAAGGTGCGGCTGCATATGCA	2460
Db	2401	GGCCATCTACAGCCCCCTACTGTTAGGGGACAGGACTAAGGTGCGGCTGCATATGCA	2460
Qy	2461	GGCCAGGGTATAAGGTGCTTGTCCTGAACCCGTCGTCGCCGCCACCTTAGTTTCGGG	2520
Db	2461	GGCCAGGGTATAAGGTGCTTGTCCTGAACCCGTCGTCGCCGCCACCTTAGTTTCGGG	2520
Qy	2521	GGGTATGTCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGCCATC	2580
Db	2521	GGGTATGTCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGCCATC	2580
Qy	2581	ACCAGGTTGCCCCCATCAGCTACTCCACCTATGGCAAGTTCTTGCGGACGGTGTGC	2640
Db	2581	ACCAGGTTGCCCCCATCAGCTACTCCACCTATGGCAAGTTCTTGCGGACGGTGTGC	2640
Qy	2641	TCTGGGGCGCTATGACATCATATATGTATGATGCTCACTCACTGACCTGACCGACCT	2700
Db	2641	TCTGGGGCGCTATGACATCATATATGTATGATGCTCACTCACTGACCTGACCGACCT	2700
Qy	2701	ATCCTGGGCATCGGCACAGTCTGGAACGAGGACGGCTGGAGCGGACTCGTCGTG	2760
Db	2701	ATCCTGGGCATCGGCACAGTCTGGAACGAGGACGGCTGGAGCGGACTCGTCGTG	2760
Qy	2761	CTCGCACCGCTAGCGCTCCGGGATCGGTCAACGTCGACCGGTGGAGCGGACTCGTCGTG	2820
Db	2761	CTCGCACCGCTAGCGCTCCGGGATCGGTCAACGTCGACCGGTGGAGCGGACTCGTCGTG	2820
Qy	2821	GCTCTGTCAGCATGGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC	2880
Db	2821	GCTCTGTCAGCATGGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC	2880
Qy	2881	AAGGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG	2940

Db	2881	AAGGGGGGAGGACCTCATTTTCTGCGCATTTCCAGAGAAATGTGATGAGCTCGCGCG	2940	Qy	4021	TGAAATTTTCATCAGCGGGATACAATAATTTAGCAGGCTTGTCTCACTCTGCTCGCAACCCC	4080
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGTCTGTAGCATATTTACCGGGCCCTTGATGTATCCGTC	3000	Db	4021	TGAAATTTTCATCAGCGGGATACAATAATTTAGCAGGCTTGTCTCACTCTGCTCGCAACCCC	4080
Db	2941	AAGCTGTCCGGCTCGGACTCAATGTCTGTAGCATATTTACCGGGCCCTTGATGTATCCGTC	3000	Qy	4081	GCATAGCATCACTGATGGCAATTCACAGCCTCTATACACAGCCGCTCACACCAACAT	4140
Qy	3001	ATACCAACTAGCGAGAGCGTCAATGTCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC	3060	Db	4081	GCATAGCATCACTGATGGCAATTCACAGCCTCTATACACAGCCGCTCACACCAACAT	4140
Db	3001	ATACCAACTAGCGAGAGCGTCAATGTCTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC	3060	Qy	4141	ACCTCTCTGTAAACATCTCTGGGGGATGGGTGCGCCCACTTGTCTCTCCAGCGCT	4200
Qy	3061	GGCGATTTCCAGTTCAGTGTACGATGCAATGTCACCAATGTCACAGAGTTCAGCTCAGC	3120	Db	4141	ACCTCTCTGTAAACATCTCTGGGGGATGGGTGCGCCCACTTGTCTCTCCAGCGCT	4200
Db	3061	GGCGATTTCCAGTTCAGTGTACGATGCAATGTCACCAATGTCACAGAGTTCAGCTCAGC	3120	Qy	4201	GCTTCTGCTTTCGTAGGCGCGCATCGCTGGAGCGGCTGTGTGGCAGCATAGGCGCTTGG	4260
Qy	3121	CTGGACCCGACTTCAACATTTAGACGACGACCGTGCACCAAGACGCGGTGTACGCTCG	3180	Db	4201	GCTTCTGCTTTCGTAGGCGCGCATCGCTGGAGCGGCTGTGTGGCAGCATAGGCGCTTGG	4260
Db	3121	CTGGACCCGACTTCAACATTTAGACGACGACCGTGCACCAAGACGCGGTGTACGCTCG	3180	Qy	4261	AAGTGTCTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGCGCGCTCGTGCC	4320
Qy	3181	CAGCGGCGAGGACGAGCTGGTGGGCGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240	Db	4261	AAGTGTCTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGCGCGCTCGTGCC	4320
Db	3181	CAGCGGCGAGGACGAGCTGGTGGGCGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240	Qy	4321	TTTAAAGTTCATGAGCGCGGATGCCCTCCACCGAGGACCTGGCTAACTACTCTCTGCT	4380
Qy	3241	GAAAGGCGCTCGGCACTTCCGATTCCTCGGTTCTGTGGAGTGTATGACGGGGCTGT	3300	Db	4321	TTTAAAGTTCATGAGCGCGGATGCCCTCCACCGAGGACCTGGCTAACTACTCTCTGCT	4380
Db	3241	GAAAGGCGCTCGGCACTTCCGATTCCTCGGTTCTGTGGAGTGTATGACGGGGCTGT	3300	Qy	4381	ATCTCTCTCTTCTGCGGCTAGTCTGCGGGGTGTGTGCGCAGCATATCTGCGTCGAC	4440
Qy	3301	GCTTGGTACGAGCTCACGCCGCCCGAGACCTCAGTTAGTTGCGGGCTTACTAAACACA	3360	Db	4381	ATCTCTCTCTTCTGCGGCTAGTCTGCGGGGTGTGTGCGCAGCATATCTGCGTCGAC	4440
Db	3301	GCTTGGTACGAGCTCACGCCGCCCGAGACCTCAGTTAGTTGCGGGCTTACTAAACACA	3360	Qy	4441	GTGGGCCACAGGGAGGGGGCTGTGAGTGTGATGAACCGGCTGATAGCGTTGCTTTCGCG	4500
Qy	3361	CCAGGGTTCGCGTCTGCGAGACGATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTTC	3420	Db	4441	GTGGGCCACAGGGAGGGGGCTGTGAGTGTGATGAACCGGCTGATAGCGTTGCTTTCGCG	4500
Db	3361	CCAGGGTTCGCGTCTGCGAGACGATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTTC	3420	Qy	4501	GATTAACAGCTCTCCCGCACGACCTATGTGCTGAGAGCGACGCTGACGACGTGTCACT	4560
Qy	3421	ACCCATAGAGCGCCATTTCTGTCCAGATTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Db	4501	GATTAACAGCTCTCCCGCACGACCTATGTGCTGAGAGCGACGCTGACGACGTGTCACT	4560
Db	3421	ACCCATAGAGCGCCATTTCTGTCCAGATTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Qy	4561	CAGATCTCTCTAGTCTTACCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACT	4620
Qy	3481	CTGTAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT	3540	Db	4561	CAGATCTCTCTAGTCTTACCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACT	4620
Db	3481	CTGTAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT	3540	Qy	4621	GAGGACTGTCTCCAGCCATGCTCCGGCTGTGCTTGAAGAGATGTTTGGGATTTGATGCT	4680
Qy	3541	CAAAATGTGAAGTGTCTATACGCTAAAGCTTACGCTGACGCGGCGCAACGCTGCTG	3600	Db	4621	GAGGACTGTCTCCAGCCATGCTCCGGCTGTGCTTGAAGAGATGTTTGGGATTTGATGCT	4680
Db	3541	CAAAATGTGAAGTGTCTATACGCTAAAGCTTACGCTGACGCGGCGCAACGCTGCTG	3600	Qy	4681	ACGCTGTTCAGTGTATTTCAAGACCTGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	4740
Qy	3601	TATAGGCTGGAGCGGCTTCAAAACGAGGTTACTACACACACCCCATAAACCAATACATC	3660	Db	4681	ACGCTGTTCAGTGTATTTCAAGACCTGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	4740
Db	3601	TATAGGCTGGAGCGGCTTCAAAACGAGGTTACTACACACACCCCATAAACCAATACATC	3660	Qy	4741	GTCCCCCTTCTCTCATGTCAACGTTGGGTCAAGGGAGTCTGCGGGGCGACGCGATCATG	4800
Qy	3661	ATGGCATGCAATGTCCGCTGACCTGGAGTGTCTCAGGACACCTGGGTGTGTTAGGGGA	3720	Db	4741	GTCCCCCTTCTCTCATGTCAACGTTGGGTCAAGGGAGTCTGCGGGGCGACGCGATCATG	4800
Db	3661	ATGGCATGCAATGTCCGCTGACCTGGAGTGTCTCAGGACACCTGGGTGTGTTAGGGGA	3720	Qy	4801	CAAAACACCTGCGCCATGTGGAGCAGATCACCGGACATGTGAAAGGTTTCCATGAGG	4860
Qy	3721	GTCTAGCAGCTGTGGCGGCTATTGCTGACAGCAGGAGCGTGTCTATTGTTGGGAGG	3780	Db	4801	CAAAACACCTGCGCCATGTGGAGCAGATCACCGGACATGTGAAAGGTTTCCATGAGG	4860
Db	3721	GTCTAGCAGCTGTGGCGGCTATTGCTGACAGCAGGAGCGTGTCTATTGTTGGGAGG	3780	Qy	4861	ATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGCATGGAAATTTCCCATTAACGGGTAC	4920
Qy	3781	ATCATCTTGTCCGGAAGCGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC	3840	Db	4861	ATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGCATGGAAATTTCCCATTAACGGGTAC	4920
Db	3781	ATCATCTTGTCCGGAAGCGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC	3840	Qy	4921	ACCAAGGCGGCTGTGACGCGCTCCCGGCGCCAAATTTATTTCTAGGGGCTGTGGCGGTG	4980
Qy	3841	GATGAGATGGAAGAGTGGGCTTACACTCTCTTATATGAAACAGGGAATGACGCTGCC	3900	Db	4921	ACCAAGGCGGCTGTGACGCGCTCCCGGCGCCAAATTTATTTCTAGGGGCTGTGGCGGTG	4980
Db	3841	GATGAGATGGAAGAGTGGGCTTACACTCTCTTATATGAAACAGGGAATGACGCTGCC	3900	Qy	4981	GCTGCTGAGGATACGTTGAGGTTTACCGGGTGGGGATTTCCACTACGTTGACGGGATG	5040
Qy	3901	GAAACAATTCACAGAGGCAATCGGTTGCTGAAACAGCCACCAAGCAAGCGAGGCT	3960	Db	4981	GCTGCTGAGGATACGTTGAGGTTTACCGGGTGGGGATTTCCACTACGTTGACGGGATG	5040
Db	3901	GAAACAATTCACAGAGGCAATCGGTTGCTGAAACAGCCACCAAGCAAGCGAGGCT	3960	Qy	5041	ACCACTGACAACTGTAAGTGCCTGTGCAAGTTCGCGGCCCGGAAATTTCTTACAGAAATG	5100
Qy	3961	GCTGCTCCCGTGGTGGAAATTCAGTGGCGGACCTCTGAAAGCTTCTGCGCGCAAGCATG	4020	Db	5041	ACCACTGACAACTGTAAGTGCCTGTGCAAGTTCGCGGCCCGGAAATTTCTTACAGAAATG	5100
Db	3961	GCTGCTCCCGTGGTGGAAATTCAGTGGCGGACCTCTGAAAGCTTCTGCGCGCAAGCATG	4020				

QY	5101	GATGGGTGCGGTTCACAGGTACGCTCAGCGTGCAAAACCCCTCCTACGGAGAGGTC	5160		Db	6181	GTGCTCAAGGAGATGAAGCGAAGCGCTCCACAGTTAAGGCTTAAACTTCTATCCGTTGGAG	6240	
Db	5101	GATGGGTGCGGTTCACAGGTACGCTCAGCGTGCAAAACCCCTCCTACGGAGAGGTC	5160		QY	6241	GAAAGCTGTAAAGCTCAGCGCCCAATTCGGCCAGATCTAAATTTGGCTATCGGGCAAG	6300	
QY	5161	ACATTCCTGGTGGGTCAATCAATACCTGGTTGGTTCACAGCTCCATTCGAGCCCGAA	5220		Db	6241	GAAAGCTGTAAAGCTCAGCGCCCAATTCGGCCAGATCTAAATTTGGCTATCGGGCAAG	6300	
Db	5161	ACATTCCTGGTGGGTCAATCAATACCTGGTTGGTTCACAGCTCCATTCGAGCCCGAA	5220		QY	6301	GACGTCCGGAACCTTATCCAGCAAGCGCTTAAACCAATCCGCTCGGTGGGAAGACTTG	6360	
QY	5221	CCGACGTAGAGTCTCACTTCCATGTCTACCGACCCCTCCCAATTCGCGGAGAGC	5280		Db	6301	GACGTCCGGAACCTTATCCAGCAAGCGCTTAAACCAATCCGCTCGGTGGGAAGACTTG	6360	
Db	5221	CCGACGTAGAGTCTCACTTCCATGTCTACCGACCCCTCCCAATTCGCGGAGAGC	5280		QY	6361	CTGGAAGACATGAGACACCAATTCGACACCAATTCATGGCAAAATATGAGTTTCTGC	6420	
QY	5281	GCTAAGCGTAGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340		Db	6361	CTGGAAGACATGAGACACCAATTCGACACCAATTCATGGCAAAATATGAGTTTCTGC	6420	
Db	5281	GCTAAGCGTAGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340		QY	6421	GTCCAAACAGAGAAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCGCAATTTGGG	6480	
QY	5341	CTGTCTGGCCCTTCCTTGAAGGCAACATGCACTACCGTCTATGCTCCCGGAGCTGAC	5400		Db	6421	GTCCAAACAGAGAAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCGCAATTTGGG	6480	
Db	5341	CTGTCTGGCCCTTCCTTGAAGGCAACATGCACTACCGTCTATGCTCCCGGAGCTGAC	5400		QY	6481	GTTCTGTGTGCGAGAAATGGCCCTTTTACGATGTGTCTCCACCTCCCTCAGCCCTG	6540	
QY	5401	CTCATCGAGGCAACCTCTGTGGCGCAGGAGATGGCGGGAACATCACCCGGTGGAG	5460		Db	6481	GTTCTGTGTGCGAGAAATGGCCCTTTTACGATGTGTCTCCACCTCCCTCAGCCCTG	6540	
Db	5401	CTCATCGAGGCAACCTCTGTGGCGCAGGAGATGGCGGGAACATCACCCGGTGGAG	5460		QY	6541	ATGGGCTCTTTCATACGGAATTCCTTACGATGTGTCTCCACCTCCCTCAGCCCTG	6600	
QY	5461	TCAGAAATAGGTAGTAAATTTTGGACTCTTTTGGAGCGCTTCCAGCGGAGGATGAG	5520		Db	6541	ATGGGCTCTTTCATACGGAATTCCTTACGATGTGTCTCCACCTCCCTCAGCCCTG	6600	
Db	5461	TCAGAAATAGGTAGTAAATTTTGGACTCTTTTGGAGCGCTTCCAGCGGAGGATGAG	5520		QY	6601	GCCTGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCCCTGTTTGAATCA	6660	
QY	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCAGGAATTTCCCTCGAGCGATG	5580		Db	6601	GCCTGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCCCTGTTTGAATCA	6660	
Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCAGGAATTTCCCTCGAGCGATG	5580		QY	6661	ACGGTCTCAGGAATGACATCCGTTGTGGAGTCAATCTTACCAATCTACATGTTGACTCA	6720	
QY	5581	CCCATATGGGCAACCGCGGATTAACCCCTCCATCTGTAGAGTCTTGGAAAGACCCGGAC	5640		Db	6661	ACGGTCTCAGGAATGACATCCGTTGTGGAGTCAATCTACCAATCTACATGTTGACTCA	6720	
Db	5581	CCCATATGGGCAACCGCGGATTAACCCCTCCATCTGTAGAGTCTTGGAAAGACCCGGAC	5640		QY	6721	CCGGAAGCCAGACAGGCCATTAAGGCTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780	
QY	5641	TACGTCCTCCAGTGTACAGGGGTTCATGCGGCTGCCAAGGCCCTCCGATACCA	5700		Db	6721	CCGGAAGCCAGACAGGCCATTAAGGCTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780	
Db	5641	TACGTCCTCCAGTGTACAGGGGTTCATGCGGCTGCCAAGGCCCTCCGATACCA	5700		QY	6781	ACTAATTTTAAAGGGCAGAACTCGCGCTATCGCGGTTCGCGCGAGCGGTGACTGAGC	6840	
QY	5701	CCTTCCAGGAGGAGAGCGGTTCCTGTCAAGATCTACCGTGTCTTCTGCTTGGG	5760		Db	6781	ACTAATTTTAAAGGGCAGAACTCGCGCTATCGCGGTTCGCGCGAGCGGTGACTGAGC	6840	
Db	5701	CCTTCCAGGAGGAGAGCGGTTCCTGTCAAGATCTACCGTGTCTTCTGCTTGGG	5760		QY	6841	ACCAGTCCGCTAATACCTCTACATGTTTAAAGCGCGCTCGCGCTTCGCGCGAGCGGTG	6900	
QY	5761	GAGTCCGCAAAAGACCTTGGCAGCTCCGAATCTGCGCGCTTCGACAGCGGCA	5820		Db	6841	ACCAGTCCGCTAATACCTCTACATGTTTAAAGCGCGCTTCGCGCTTCGCGCGAGCGGTG	6900	
Db	5761	GAGTCCGCAAAAGACCTTGGCAGCTCCGAATCTGCGCGCTTCGACAGCGGCA	5820		QY	6901	AAAGTCCAGGACTGACGATGCTCGTATCGGAGACGACCTTGTCTGTGAAAGC	6960	
QY	5821	ACGGCTCTCTGACCGACCTCCGACGAGCGGATCCGAGCTCCGAGCTTGAATCGTAC	5880		Db	6901	AAAGTCCAGGACTGACGATGCTCGTATCGGAGACGACCTTGTCTGTGAAAGC	6960	
Db	5821	ACGGCTCTCTGACCGACCTCCGACGAGCGGATCCGAGCTCCGAGCTTGAATCGTAC	5880		QY	6961	GGGGGACCCAAAGAGACGAGCGGAGCTTACGGGCTTTCACGGAGCTATGACTAGATAC	7020	
QY	5881	TCCTCCATGCCCCCTTGGAGGGAGCCGGGGATCCCGATCTCAGCGAGGCTTGG	5940		Db	6961	GGGGGACCCAAAGAGACGAGCGGAGCTTACGGGCTTTCACGGAGCTATGACTAGATAC	7020	
Db	5881	TCCTCCATGCCCCCTTGGAGGGAGCCGGGGATCCCGATCTCAGCGAGGCTTGG	5940		QY	7021	TCCTCCATGTTGTCAGTCGCGCACGATGCTATCGGAGACGACCTTGTCTGTGAAAGC	7080	
QY	5941	TCTACCGTAAGCGAGAGCTAGTGAAGAGCTGCTGCTGCTCGATGCTTACACATGG	6000		Db	7021	TCCTCCATGTTGTCAGTCGCGCACGATGCTATCGGAGACGACCTTGTCTGTGAAAGC	7080	
Db	5941	TCTACCGTAAGCGAGAGCTAGTGAAGAGCTGCTGCTGCTCGATGCTTACACATGG	6000		QY	7081	TCCTCCATGTTGTCAGTCGCGCACGATGCTATCGGAGACGACCTTGTCTGTGAAAGC	7140	
QY	6001	ACAGCGCCCTGATCAGCCATGCGCTGGGAGGAAACCAAGCTGCCATCAATGACTG	6060		Db	7081	TCCTCCATGTTGTCAGTCGCGCACGATGCTATCGGAGACGACCTTGTCTGTGAAAGC	7140	
Db	6001	ACAGCGCCCTGATCAGCCATGCGCTGGGAGGAAACCAAGCTGCCATCAATGACTG	6060		QY	7141	GACCCCAACCCCTTGGCGGGGCTGCGTGGGAGACGACTAGACACATCCAGTCAAT	7200	
QY	6061	AGCAACTCTTGTCCGTCACCAACCTTGTCTATGCTACCAATCTCGCAGCGCAAGC	6120		Db	7141	GACCCCAACCCCTTGGCGGGGCTGCGTGGGAGACGACTAGACACATCCAGTCAAT	7200	
Db	6061	AGCAACTCTTGTCCGTCACCAACCTTGTCTATGCTACCAATCTCGCAGCGCAAGC	6120		QY	7201	TCCTGGCTAGGCAACATCATCATGATGTCGCCACCTTGTGGGCAAGGATCATCTGATG	7260	
QY	6121	CTGGCGAGAGAGGTCACCTTTGACAGACTGACAGTCTGAGGTCCTGGAGCAGCACTACCGGGAC	6180		Db	7201	TCCTGGCTAGGCAACATCATCATGATGTCGCCACCTTGTGGGCAAGGATCATCTGATG	7260	
Db	6121	CTGGCGAGAGAGGTCACCTTTGACAGACTGACAGTCTGAGGTCCTGGAGCAGCACTACCGGGAC	6180		QY	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACCTTGAAGGCTTAACTTCTATCCGTTGGAG	7320	
QY	6181	GTGCTCAGGAGATGAAGCGGAGCGCTCCACAGTTAAGGCTTAACTTCTATCCGTTGGAG	6240						

Db 7261 ACTCATTTCTTCCATCTCTAGCTCAGGAACAACCTGAAAGGCCCTAGATTCTCAG 7320
 QY 7321 ATCTAGGGGCGCTTACTCCATTTGAGCCACTTGAACCTCAGATCAATCAAGACTC 7380
 Db 7321 ATCTAGGGGCGCTTACTCCATTTGAGCCACTTGAACCTCAGATCAATCAAGACTC 7380
 QY 7381 CATGGCCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
 Db 7381 CATGGCCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
 QY 7441 TCATGCTCAGGAAACTTGGGCTACCGCTTGGAGTCTGGAGACATCGGGCCAGAACT 7500
 Db 7441 TCATGCTCAGGAAACTTGGGCTACCGCTTGGAGTCTGGAGACATCGGGCCAGAACT 7500
 QY 7501 GTCCGCGTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTCTC 7560
 Db 7501 GTCCGCGTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTCTC 7560
 QY 7561 AACTGGGCGAGTAAGGACCAAGCTCAACTCACTCCATCCCGCTGGCTGCCAGTTGGAT 7620
 Db 7561 AACTGGGCGAGTAAGGACCAAGCTCAACTCACTCCATCCCGCTGGCTGCCAGTTGGAT 7620
 QY 7621 TTATCCAGCTGGTTCGTTGCTGCTTACAGCGGGGAGACATATATCAAGCCTGTCTCGT 7680
 Db 7621 TTATCCAGCTGGTTCGTTGCTGCTTACAGCGGGGAGACATATATCAAGCCTGTCTCGT 7680
 QY 7681 GCGGACCCCGCTGGTTCATGTGTGCTTACTCTTCTTCTGTAAGGGTAGGCATCTAT 7740
 Db 7681 GCGGACCCCGCTGGTTCATGTGTGCTTACTCTTCTTCTGTAAGGGTAGGCATCTAT 7740
 QY 7741 CTACTCCCAACCGAGTAAGGAGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTTTT 7800
 Db 7741 CTACTCCCAACCGAGTAAGGAGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTTTT 7800
 QY 7801 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 Db 7801 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 QY 7861 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
 Db 7861 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
 QY 7921 TAGCTGTGAAGGTCGCTGAGCGCTTGAAGTCTGAGAGAGTCTGATAGTCTCTCTGC 7980
 Db 7921 TAGCTGTGAAGGTCGCTGAGCGCTTGAAGTCTGAGAGAGTCTGATAGTCTCTCTGC 7980
 QY 7981 AGATCAAGTACT 7992
 Db 7981 AGATCAAGTACT 7992

RESULT 4
 AD83762
 ID AD83762 standard; DNA; 10690 BP.
 XX
 AC AD83762;
 XX
 DT 01-JAN-2004 (first entry)
 XX pHVNeol7.wt plasmid containing an HCV bicistronic replicon.
 DE
 XX Hepatitis C virus; thiosemicarbazone;
 KW 4-(cinnamyl)oxy)benzaldehyde thiosemicarbazone; RHEPLISA; Ia; hepatitis C;
 KW HCV replication system; bicistronic RNA replicon;
 KW neomycin phosphotransferase; human hepatoma cell line; Huh-7;
 KW neomycin sulphate; G418; pHVNeol7.wt; replicon 1377neo/NS3-3; wt.;
 KW hepatotropic; virucide; antiinflammatory; ds.
 XX
 OS Synthetic.
 OS Unidentified.
 OS Hepatitis C virus.
 XX
 FN US2003176503-A1.

XX 18-SEP-2003.
 XX 19-APR-2002; 2002US-00125920.
 XX 20-APR-2001; 2001US-0295195P.
 XX (ALTA/) ALTAMURA S.
 XX (KOCH/) KOCH U.
 XX Altamura S, Koch U;
 XX WPI; 2003-778475/73.
 XX Use of thiosemicarbazone compounds for e.g. treating and preventing
 XX hepatitis C or its related condition, and delaying the onset of hepatitis
 XX C or its related condition.
 XX Example 3; SEQ ID NO 1; 30pp; English.
 XX The invention discloses a method for the treatment and prevention of
 XX hepatitis C, or its related condition, which involves the administration
 XX of thiosemicarbazone compounds, or its salts. The inhibitory activity of
 XX 4-(cinnamyl)oxy)benzaldehyde thiosemicarbazone was evaluated using
 XX RHEPLISA assay in a 96-well microplate format. The route of
 XX administration is oral, parenteral (e.g. subcutaneous, intravenous,
 XX intramuscular, intrasternal injection, or infusion), by inhalation spray
 XX or rectal. The use of the 35 compounds disclosed is specifically claimed,
 XX e.g. 4-(cinnamyl)oxy)benzaldehyde thiosemicarbazone (Ia). The compounds
 XX are useful for treating and preventing hepatitis C or its related
 XX condition, delaying the onset of hepatitis C or its related condition and
 XX inhibiting replication of the hepatitis C virus. HCV replication
 XX inhibitor of replication of the hepatitis C virus. Selection of cells
 XX systems can be obtained using various techniques. Selection of cells
 XX capable of supporting HCV replication can be achieved using bicistronic
 XX RNA replicons expressing a selectable marker, the neomycin
 XX phosphotransferase. Transfection of these replicons in the human hepatoma
 XX cell line, Huh-7, followed by isolation of clones that support HCV
 XX sulphate (G418), permits the isolation of clones that support HCV
 XX replication. The sequence presented is the pHVNeol7.wt plasmid which
 XX contains the CDNA coding for an HCV bicistronic replicon identical to
 XX replicon 1377neo/NS3-3/wt.
 XX
 XX Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
 Query Match 99.9%; Score 7985.6; DB 9; Length 10690;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
 Db 1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
 QY 61 TCTTACGCGAGAAGCGTCTAGCCATGGGCTTAGTATGATGATGATGATGATGATGATGAT 120
 Db 61 TCTTACGCGAGAAGCGTCTAGCCATGGGCTTAGTATGATGATGATGATGATGATGATGAT 120
 QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTCGCG 180
 Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTCGCG 180
 QY 181 GAGACCGGTCTCTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGCGCTGCCCCC 240
 Db 181 GAGACCGGTCTCTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGCGCTGCCCCC 240
 QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGTTCGCGAAGGCCCTTGTGTACTGCTGATAGG 300
 Db 241 GCGAGACTGCTAGCCGAGTAGTGTGGTTCGCGAAGGCCCTTGTGTACTGCTGATAGG 300
 QY 301 GTGCTTCGAGTGCCTCCGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCCTAAAC 360
 Db 301 GTGCTTCGAGTGCCTCCGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCCTAAAC 360

QY 361 CTCAGAGAAAACAAAGGGCGCGCCATGATTGAACAAGATGAATTGACGAGGTTCTC 420
Db |||||
QY 361 CTCAGAGAAAACAAAGGGCGCGCCATGATTGAACAAGATGAATTGACGAGGTTCTC 420
Db |||||
QY 421 CGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCAACAAGCAATCGCGTCT 480
Db |||||
QY 421 CGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCAACAAGCAATCGCGTCT 480
Db |||||
QY 481 CTGATGCCCGCTGTTCGGGCTGTGAGCGACAGGGCGCCCGTCTCTTTTGTGCAAGACG 540
Db |||||
QY 481 CTGATGCCCGCTGTTCGGGCTGTGAGCGACAGGGCGCCCGTCTCTTTTGTGCAAGACG 540
Db |||||
QY 541 ACCTGTCCGGTGCCTGAATGAATGACGAGCAGGCGAGCGGCTATCGTGGCTGGCCA 600
Db |||||
QY 541 ACCTGTCCGGTGCCTGAATGAATGACGAGCAGGCGAGCGGCTATCGTGGCTGGCCA 600
Db |||||
QY 601 CGAGGGGCTTCCCTTGGCGAGCTGTCTGAGCTGCTGAGCTGTCTCACTGAAGCGGGAAGGACTGGC 660
Db |||||
QY 601 CGAGGGGCTTCCCTTGGCGAGCTGTCTGAGCTGCTGAGCTGTCTCACTGAAGCGGGAAGGACTGGC 660
Db |||||
QY 661 TGCTATTGGGCAAGTGCAGGAGGATCTCCTGTCTATCTCACTTGTCTCTCCCGAGA 720
Db |||||
QY 661 TGCTATTGGGCAAGTGCAGGAGGATCTCCTGTCTATCTCACTTGTCTCTCCCGAGA 720
Db |||||
QY 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGGCTACCTGCC 780
Db |||||
QY 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGGCTACCTGCC 780
Db |||||
QY 781 CATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAAGTCTCGATGGAAGCGGTC 840
Db |||||
QY 781 CATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAAGTCTCGATGGAAGCGGTC 840
Db |||||
QY 841 TTGTGATACGAGTGTCTGGAAGAGATCAGGGGCTCGCGGAGCATCTCGTGAACCATGGGATGCCT 960
Db |||||
QY 841 TTGTGATACGAGTGTCTGGAAGAGATCAGGGGCTCGCGGAGCATCTCGTGAACCATGGGATGCCT 960
Db |||||
QY 901 CCAAGCTCAAGGCGGATCCCGAAGAGATCTCGTGAACCATGGGATGCCT 960
Db |||||
QY 901 CCAAGCTCAAGGCGGATCCCGAAGAGATCTCGTGAACCATGGGATGCCT 960
Db |||||
QY 961 GCTTTCGGAATATCATGGTGGAAATGGCGCTTTCTGATTCATCGATCGATGGCGGC 1020
Db |||||
QY 961 GCTTTCGGAATATCATGGTGGAAATGGCGCTTTCTGATTCATCGATCGATGGCGGC 1020
Db |||||
QY 1021 TGGGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATTTCTGGAATCATCGA 1080
Db |||||
QY 1021 TGGGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATTTCTGGAAGC 1080
Db |||||
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTCGTCTTACGGTATCGGATCGCGCTCCCGATTGCG 1140
Db |||||
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTCGTCTTACGGTATCGGATCGCGCTCCCGATTGCG 1140
Db |||||
QY 1141 AGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAAG 1200
Db |||||
QY 1141 AGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAAG 1200
Db |||||
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTCAACGTTACTGCG 1260
Db |||||
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTCAACGTTACTGCG 1260
Db |||||
QY 1261 CGAAGCGCTTGAATAGGCGGCTGTGGTGTGCTATATGTTATTTTCCACCATATTG 1320
Db |||||
QY 1261 CGAAGCGCTTGAATAGGCGGCTGTGGTGTGCTATATGTTATTTTCCACCATATTG 1320
Db |||||
QY 1321 CGCTTTTGGCAATGTGAGGCGCCGGAACCTGGCCCTGTCTTCTGACGAGCATTCCT 1380
Db |||||
QY 1321 CGCTTTTGGCAATGTGAGGCGCCGGAACCTGGCCCTGTCTTCTGACGAGCATTCCT 1380
Db |||||
QY 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAAATGCTGTAAGGAAGCA 1440
Db |||||
QY 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAAATGCTGTAAGGAAGCA 1440
Db |||||
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAAGTCTGTAGCGACCTTTTGCAGGCGG 1500
Db |||||

Db |||||
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAAGTCTGTAGCGACCTTTTGCAGGACGG 1500
Db |||||
QY 1501 AACCCCGCCACCTGGCGACAGGTGCCTCTCGGCGCAAAAGCCACGCTGATATAAGATACCT 1560
Db |||||
QY 1501 AACCCCGCCACCTGGCGACAGGTGCCTCTCGGCGCAAAAGCCACGCTGATATAAGATACCT 1560
Db |||||
QY 1561 GCAAGGGCGGCAACCCCGAGTGCACCTGTGTGAGTGTGATGTTGTGAAAGAGTCAAA 1620
Db |||||
QY 1561 GCAAGGGCGGCAACCCCGAGTGCACCTGTGTGAGTGTGATGTTGTGAAAGAGTCAAA 1620
Db |||||
QY 1621 TGGCTCTCTCAAGGCTATTCAAAAGGGCTGAAAGATGCCAGAGGTACCCATTTGT 1680
Db |||||
QY 1621 TGGCTCTCTCAAGGCTATTCAAAAGGGCTGAAAGATGCCAGAGGTACCCATTTGT 1680
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QY 1681 ATGGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTTAGTCGAGGTTAAAA 1740
Db |||||
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Db |||||
QY 1741 AACGTCATAGGCTTGGGCTTCCGAAACCAAGGGCTGAAAGATGCCAGAGGTAAAA 1800
Db |||||
QY 1741 AACGTCATAGGCTTGGGCTTCCGAAACCAAGGGCTGAAAGATGCCAGAGGTAAAA 1800
Db |||||
QY 1801 ATGGGCTTATAGGCTTCTCCAAAGAGAGGCTTCTTGGCTGATCATCACT 1860
Db |||||
QY 1801 ATGGGCTTATAGGCTTCTCCAAAGAGAGGCTTCTTGGCTGATCATCACT 1860
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QY 1861 AGCTCAGAGCGGAGACAGAACCCAGTGCAGGGGAGGTCCAGGTGGTCTCCACGCA 1920
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QY 1861 AGCTCAGAGCGGAGACAGAACCCAGTGCAGGGGAGGTCCAGGTGGTCTCCACGCA 1920
Db |||||
QY 1921 ACACATCTTCTGGGCTCTCGTCAATGGGCTGTGTGGAGTCTCTATCATGTGGC 1980
Db |||||
QY 1921 ACACATCTTCTGGGCTCTCGTCAATGGGCTGTGTGGAGTCTCTATCATGTGGC 1980
Db |||||
QY 1981 GGTCTCAAGACCTTGGCGGCTTCCGAGGCTTCCAGTGGTCTATCATGTGGC 2040
Db |||||
QY 1981 GGTCTCAAGACCTTGGCGGCTTCCGAGGCTTCCAGTGGTCTATCATGTGGC 2040
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QY 2041 CAGGACTCTCGCTGGCAAGCGCCCGCGGGCGGTCTTGCACCATGACCTGC 2100
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QY 2041 CAGGACTCTCGCTGGCAAGCGCCCGCGGGCGGTCTTGCACCATGACCTGC 2100
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QY 2101 GGAGCTCGGACTTACTTGGTCAAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 2160
Db |||||
QY 2101 GGAGCTCGGACTTACTTGGTCAAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 2160
Db |||||
QY 2161 GGCGACAGAGGAGGAGCTTCTCCCGAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 2220
Db |||||
QY 2161 GGCGACAGAGGAGGAGCTTCTCCCGAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 2220
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QY 2221 GGCGGCTCACTGCTCTGCGGCTCGGGGACGCTTGTGGGCTTCCAGGCTTCCAGGCT 2280
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QY 2401 GCCCATCTACAGCGGCTTGTGTAGCGGCAAGAGCACTAAGGTCGCGCTCGATGCA 2460
Db |||||
QY 2401 GCCCATCTACAGCGGCTTGTGTAGCGGCAAGAGCACTAAGGTCGCGCTCGATGCA 2460
Db |||||
QY 2461 GCCCAAGGCTAAGGCTTGTGTGTGAAACCGCTCGCGGCTTCCAGGCTTCCAGGCT 2520
Db |||||
QY 2461 GCCCAAGGCTAAGGCTTGTGTGTGAAACCGCTCGCGGCTTCCAGGCTTCCAGGCT 2520
Db |||||
QY 2521 GCGTATATGCTAAGGCTTGTGTGTGAAACCGCTTCCAGGCTTCCAGGCTTCCAGGCT 2580
Db |||||

QY 4741 GTCCCTCTCTCTCATGTCAAAGTGGGTACAGGGAGTCTGGCGGGCGACGGCATCATG 4800
Db 4741 GTCCCTCTCTCTCATGTCAAAGTGGGTACAGGGAGTCTGGCGGGCGACGGCATCATG 4800
QY 4801 CAAACACACCTGCTGAGGACACAGATCACCGGACATGTGAAGAAAGGTTCCATGAGG 4860
Db 4801 CAAACACACCTGCTGAGGACACAGATCACCGGACATGTGAAGAAAGGTTCCATGAGG 4860
QY 4861 ATCTGGGGCCCTAGGACTGTAGTAAACAGTGGCATGGAACATTCCTCCCATTAACCGGTAC 4920
Db 4861 ATCTGGGGCCCTAGGACTGTAGTAAACAGTGGCATGGAACATTCCTCCCATTAACCGGTAC 4920
QY 4921 ACCACGGGCCCTGACAGCCCTCCCGGGCCCAATATTCTAGGGCGCTGTGGGGGTG 4980
Db 4921 ACCACGGGCCCTGACAGCCCTCCCGGGCCCAATATTCTAGGGCGCTGTGGGGGTG 4980
QY 4981 GCTGCTGAGGAGTACGTGGAGGTACCGGGGTGGGGGATTTCCACTAGCTGACGGGCATG 5040
Db 4981 GCTGCTGAGGAGTACGTGGAGGTACCGGGGTGGGGGATTTCCACTAGCTGACGGGCATG 5040
QY 5041 ACCACTGACAGCTAAAGTGCCCGTGTCAAGTTCCTGGGCCCGCCGAATTTCTTACAGAAAGT 5100
Db 5041 ACCACTGACAGCTAAAGTGCCCGTGTCAAGTTCCTGGGCCCGCCGAATTTCTTACAGAAAGT 5100
QY 5101 GATGGGTGCGGTGTCACAGGTACGCTCCAGGTGCAAAACCCCTCTACGGGAGGAGTGC 5160
Db 5101 GATGGGTGCGGTGTCACAGGTACGCTCCAGGTGCAAAACCCCTCTACGGGAGGAGTGC 5160
QY 5161 ACATTCCTGTGTGGGTCAATCAATACCTGTGTGGGTGCAAGCTCCCATGCGAGCCGAA 5220
Db 5161 ACATTCCTGTGTGGGTCAATCAATACCTGTGTGGGTGCAAGCTCCCATGCGAGCCGAA 5220
QY 5221 CCGAGCTAGAGTGTCACTTCCATGTCTACCGACCCCTCCCACTTACCGGGGAGACG 5280
Db 5221 CCGAGCTAGAGTGTCACTTCCATGTCTACCGACCCCTCCCACTTACCGGGGAGACG 5280
QY 5281 GCTAAGCTAGGTGGCGAGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG 5340
Db 5281 GCTAAGCTAGGTGGCGAGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG 5340
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Db 5341 CTGTCTGCGCTCTCTTGAAGGCAACATGACATCCGCTCATGACTTCCCGGACGCTGAC 5400
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Db 5401 CTGATGAGGCCAACCCTCTGTGGCGGAGAGATGGCGGGGACATCAACCCCGTGGAG 5460
QY 5461 TCAGAAATAAGGTAGTAATTTGGACTCTTTCGAGCCGCTCCAGCGGAGGAGATGAG 5520
Db 5461 TCAGAAATAAGGTAGTAATTTGGACTCTTTCGAGCCGCTCCAGCGGAGGAGATGAG 5520
QY 5521 AGGGAAGTATCCGCTCCGGCGAGATCTCTCGGAGGTCCAGGAAATTCCTCGAGCGATG 5580
Db 5521 AGGGAAGTATCCGCTCCGGCGGAGATCTCTCGGAGGTCCAGGAAATTCCTCGAGCGATG 5580
QY 5581 CCATATGGGACCGCCGATTAACACCTTCACTGTAGAGTCTCTGGAAGGACCCCGGAC 5640
Db 5581 CCATATGGGACCGCCGATTAACACCTTCACTGTAGAGTCTCTGGAAGGACCCCGGAC 5640
QY 5641 TACGTCCCTCCAGTGGTACACGGGTGTCAATTCGCGCTGCAAGGCCCTCCGATACCA 5700
Db 5641 TACGTCCCTCCAGTGGTACACGGGTGTCAATTCGCGCTGCAAGGCCCTCCGATACCA 5700
QY 5701 CTTCAACGAGGAGGAGGAGTGTCTCTGCTCAGAAATCTACCGTGTCTCTGCTTGGG 5760
Db 5701 CTTCAACGAGGAGGAGGAGTGTCTCTGCTCAGAAATCTACCGTGTCTCTGCTTGGG 5760
QY 5761 GAGCTCGGCAACAAAGCTTCCGAGCTCCGAATCGTGGCGGTGCAAGGGGACCGCA 5820
Db 5761 GAGCTCGGCAACAAAGCTTCCGAGCTCCGAATCGTGGCGGTGCAAGGGGACCGCA 5820
QY 5821 ACGGCTCTCTCTGACAGCCCTCCGACGAGCGGAGATCCGATCGTGTGAGTCTGATC 5880

Db 5821 ACGGCTCTCTCTGACAGCCCTCCGACGAGCGGACGCGGATCCGACGTTGAGTCGTAC 5880
QY 5881 TCTCTCATCCCTCCCTTCTGAGGGGAGCGGGGATCCGATCTCAGCGACGGGTCTTGG 5940
Db 5881 TCTCTCATCCCTCCCTTCTGAGGGGAGCGGGGATCCGATCTCAGCGACGGGTCTTGG 5940
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Db 5941 TCTACCGTAAGCGAGGAGGCTAGTGAAGGACGTCGTCTGCTGCTCGATGCTCTACACATGG 6000
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Db 6061 AGCAACTCTTTGCTCCGTCACCAACACTTGGTCTATGCTACCAACATCTCGAGCGCAAGC 6120
QY 6121 CTGGGCGAAGAAAGGTCACTTTTGACAGACTGCGAGGTCTCTGGACGACCACTACCGGAC 6180
Db 6121 CTGGGCGAAGAAAGGTCACTTTTGACAGACTGCGAGGTCTCTGGACGACCACTACCGGAC 6180
QY 6181 GTGCTCAAGGAGATCAAGGCGCAAGGCTCCACAGTTAAGGCTAACTTCTATCCGTGAG 6240
Db 6181 GTGCTCAAGGAGATCAAGGCGCAAGGCTCCACAGTTAAGGCTAACTTCTATCCGTGAG 6240
QY 6241 GAAGCTCTGTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCGAAAG 6300
Db 6241 GAAGCTCTGTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCGAAAG 6300
QY 6301 GAGCTCGGAAACCTATCCAGCAAGCGGCTTAAACACATCCGCTCCGCTGCGAAGGACTG 6360
Db 6301 GAGCTCGGAAACCTATCCAGCAAGCGGCTTAAACACATCCGCTCCGCTGCGAAGGACTG 6360
QY 6361 CTGGAAGACTGAGACACCAATTGACCAACATCATGCAAAATAGGTTTTCTGCG 6420
Db 6361 CTGGAAGACTGAGACACCAATTGACCAACATCATGCAAAATAGGTTTTCTGCG 6420
QY 6421 GTCCAAACGAGAAAGGGGCGCCGACAGCTCGCTTATCGTATTCAGATTTGGGG 6480
Db 6421 GTCCAAACGAGAAAGGGGCGCCGACAGCTCGCTTATCGTATTCAGATTTGGGG 6480
QY 6481 GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCACCTCCCTCAGGCGGTG 6540
Db 6481 GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCACCTCCCTCAGGCGGTG 6540
QY 6541 ATGGGCTCTTACAGGATTCGAATCTCTCTGGAAGCGGTGAGTTCTGTGTAAT 6600
Db 6541 ATGGGCTCTTACAGGATTCGAATCTCTCTGGAAGCGGTGAGTTCTGTGTAAT 6600
QY 6601 GCTTGAAGCGAAGAAATGGCCCTATGGCTTCGCAATGACACCGCTGTTTGACTCA 6660
Db 6601 GCTTGAAGCGAAGAAATGGCCCTATGGCTTCGCAATGACACCGCTGTTTGACTCA 6660
QY 6661 ACAGTCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGTGACTGGCC 6720
Db 6661 ACAGTCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGTGACTGGCC 6720
QY 6721 CCGGAGCGGAGCGGCAATAGGTGCGTCAAGAGCGGCTTACATCGGGGCGCCCTG 6780
Db 6721 CCGGAGCGGAGCGGCAATAGGTGCGTCAAGAGCGGCTTACATCGGGGCGCCCTG 6780
QY 6781 ACTAATTTAAAGGCGAGAACTGGCGCTATCGCGGTGCGCGGAGCGGTGTACTGACG 6840
Db 6781 ACTAATTTAAAGGCGAGAACTGGCGCTATCGCGGTGCGCGGAGCGGTGTACTGACG 6840
QY 6841 ACCAGTCCGCTAATACCTCACTGTTTGAAGGCGGTGCGGCTGTCGAGCTGG 6900
Db 6841 ACCAGTCCGCTAATACCTCACTGTTTGAAGGCGGTGCGGCTGTCGAGCTGG 6900
QY 6901 AAGCTCCAGGACTGCAAGTCTGTAAGCGGAGCGACCTTGTGTTATCTGTGAAGC 6960

Db 6901 AAGCTCCAGGACTGCGATGCTGCTATGCGGAGACGACTTGTCTGTTATCTGTGAAGC 6960
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Db 7081 TCCTCCAAATGTCAGTCGCGCAGATGCTCTGCGCAAAAGGGTGTAATCTCTCACCGT 7140
Qy 7141 GACCCCAACCCCTTTCGCGGCTGCTGCGGAGACGACTAGACACACTTCCAGTCAAT 7200
Db 7141 GACCCCAACCCCTTTCGCGGCTGCTGCGGAGACGACTAGACACACTTCCAGTCAAT 7200
Qy 7201 TCCTGGCTAGCAACATCATATGATGCGGCTGCTGCGGAGACGACTAGACACACTTCCAGTCAAT 7260
Db 7201 TCCTGGCTAGCAACATCATATGATGCGGCTGCTGCGGAGACGACTAGACACACTTCCAGTCAAT 7260
Qy 7261 ACTGATTTCTTCTCCATCTTCTAGCTCAGGAACTTGAAGAGCCCTAGATTGTGAG 7320
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Db 7321 ATCTACGGGCTGTTTACTTCCATTGAGCCACTTGACCTCAGATCAATTCAGACTC 7380
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Db 7381 CATGCGCTTACGCAATTTCTCATGATGTTACTTCCAGTGGATCAATAGGTTGGCT 7440
Qy 7441 TCATGCTCAGAACTTGGGCTGACCGCTTGGAGTCTGAGACATCGGCGCAGACT 7500
Db 7441 TCATGCTCAGAACTTGGGCTGACCGCTTGGAGTCTGAGACATCGGCGCAGACT 7500
Qy 7501 GTCCGGCTAGGCTACTGTCAGGCGGAGGCTGCCACTTGTGGCAAGTACTCTTC 7560
Db 7501 GTCCGGCTAGGCTACTGTCAGGCGGAGGCTGCCACTTGTGGCAAGTACTCTTC 7560
Qy 7561 AACTGGGCTAGTAAAGCAAGCTCAATCTCCTCAATCCCGCTCGCTCCAGTTGGAT 7620
Db 7561 AACTGGGCTAGTAAAGCAAGCTCAATCTCCTCAATCCCGCTCGCTCCAGTTGGAT 7620
Qy 7621 TATTCAGTGGTTCGTTGCTGTTACAGCGGGGAGACATATACAGCCCTGCTCGT 7680
Db 7621 TATTCAGTGGTTCGTTGCTGTTACAGCGGGGAGACATATACAGCCCTGCTCGT 7680
Qy 7681 GCGCGACCCGCTGGTTCATGTTGCTGCTACTCTCTACTTCTGTTAGGGTAGGATCTAT 7740
Db 7681 GCGCGACCCGCTGGTTCATGTTGCTGCTACTCTCTACTTCTGTTAGGGTAGGATCTAT 7740
Qy 7741 CTATCTCCCAACCGATGAGCGGAGCTAACTCCAGCCCAATAGCCATCTGTTT 7800
Db 7741 CTATCTCCCAACCGATGAGCGGAGCTAACTCCAGCCCAATAGCCATCTGTTT 7800
Qy 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Qy 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Qy 7921 TAGCTGTGAAGGTCGCTGAGCCGCTGACTGCGAGAGTCTGATCTAGTGGCCCTCTGTC 7980
Db 7921 TAGCTGTGAAGGTCGCTGAGCCGCTGACTGCGAGAGTCTGATCTAGTGGCCCTCTGTC 7980
Qy 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 5

AA47281 standard; DNA; 7992 BP.

XX AAL47281;
AC AAL47281;

XX 30-AUG-2002 (first entry)

XX Hepatitis C virus sub-genomic replicon recombinant clone HCVR24.

XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
XX virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX Hepatitis C virus.

XX WO200238793-A2.

XX 16-MAY-2002.

XX 02-NOV-2001; 2001WO-US046350.

XX 07-NOV-2000; 2000US-0245866P.

XX (ANAD-) ANADYS PHARM INC.

XX Bichko V;

XX WPI; 2002-490082/52.

XX Novel nucleic acid encoding replication competent recombinant hepatitis C
virus genome useful for screening anti-hepatitis C virus therapeutics and
for vaccine development.

XX Claim 11; Page 70-75; 85pp; English.

XX The present invention provides protein and coding sequences from
Hepatitis C virus (HCV), comprising all or part of the HCV genome and
able to replicate efficiently when transfected into a susceptible cell
line without reducing the growth rate of the cell line by more than 10
fold. The sequences are useful for screening for anti-HCV therapeutics,
for detecting antibodies to HCV in a biological sample such as blood,
serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
for deriving authentic HCV components such as replication-competent non-
infectious, replication-defective infection-component, and replication-
defective non-infectious HCV, in gene therapy or gene vaccination
targeted to hepatic tissue for treating an animal infected or susceptible
to HCV infection and for studying HCV infection and propagation. The
present sequence is a clone of a fragment of the HCV genome designated
HCVR24

XX Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 U; 0 Other;

XX Query Match 99.9%; Score 7984; DB 6; Length 7992;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCCAGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
Db 1 GCCAGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
Qy 61 TCTTCACGAGAAAGCGTCTAGCATGGGTTAGTATGAGTGTCTGTCAGCTCCAGGAC 120
Db 61 TCTTCACGAGAAAGCGTCTAGCATGGGTTAGTATGAGTGTCTGTCAGCTCCAGGAC 120
Qy 121 CCCCCCTCCGGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATGCCAG 180
Db 121 CCCCCCTCCGGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATGCCAG 180
Qy 181 GACGACCGGTCCTTTCTTGTGATCAACCCGCTCAATGCTGAGATTTGGCGTGCCTCC 240
Db 181 GACGACCGGTCCTTTCTTGTGATCAACCCGCTCAATGCTGAGATTTGGCGTGCCTCC 240

QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGCGCTTGTGTACTGTGCTGATAGG 300
DB |||||
241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGCGCTTGTGTACTGTGCTGATAGG 300
QY 301 GTGCTTGGAGTGCCTCCCGGAGGTCTGTAGACCGTGCACCATGACGACGAATCCTAAAC 360
DB |||||
301 GTGCTTGGAGTGCCTCCCGGAGGTCTGTAGACCGTGCACCATGACGACGAATCCTAAAC 360
QY 361 CTCAAAGAAAACCAAGGCGCGCATGATTGAACAAGATGGATTGACGAGGTTCTC 420
DB |||||
361 CTCAAAGAAAACCAAGGCGCGCATGATTGAACAAGATGGATTGACGAGGTTCTC 420
QY 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAAGACAATCGGCTGCT 480
DB |||||
421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAAGACAATCGGCTGCT 480
QY 481 CTGATGCCGCGGTGCTCGGCTGTGAGCGAGGGCGCGCGTCTTTTTCGAAAGCCG 540
DB |||||
481 CTGATGCCGCGGTGCTCGGCTGTGAGCGAGGGCGCGCGTCTTTTTCGAAAGCCG 540
QY 541 ACCTGTCCGTCCTGATGAATCTGAGGACGAGGAGCGCGGTATCGTGGCTGGCA 600
DB |||||
541 ACCTGTCCGTCCTGATGAATCTGAGGACGAGGAGCGCGGTATCGTGGCTGGCA 600
QY 601 CGAGCGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGGACTGGC 660
DB |||||
601 CGAGCGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGGACTGGC 660
QY 661 TGTATTGGGCGAGTGCCTGGGCGAGGATCTCTGTCACTCTGCTTGTCTTTCGAGAGC 720
DB |||||
661 TGTATTGGGCGAGTGCCTGGGCGAGGATCTCTGTCACTCTGCTTGTCTTTCGAGAGC 720
QY 721 AAGTATCCATCATGCTGATGCAATGCGGCGAGGATCTCTGTCACTCTGCTTGTCTTTCG 780
DB |||||
721 AAGTATCCATCATGCTGATGCAATGCGGCGAGGATCTCTGTCACTCTGCTTGTCTTTCG 780
QY 781 CATTGACCAACCAAGCGAAACATCGCATCGAGCGACGATCTCGGATGGAAGCGGTC 840
DB |||||
781 CATTGACCAACCAAGCGAAACATCGCATCGAGCGACGATCTCGGATGGAAGCGGTC 840
QY 841 TTGTCGATCAGATGATCTGGAAGAGATCAGGGGTGCGCCAGCGCAACTGTTCG 900
DB |||||
841 TTGTCGATCAGATGATCTGGAAGAGATCAGGGGTGCGCCAGCGCAACTGTTCG 900
QY 901 CCAGGCTCAAGGCGCGCATGCGCGAGGATCTCGTGTGACCCATGGCGATGCGCT 960
DB |||||
901 CCAGGCTCAAGGCGCGCATGCGCGAGGATCTCGTGTGACCCATGGCGATGCGCT 960
QY 961 GCTTGCAGATATCATGTTGGGAAATGGCCGCTTTTCTGGAATCATCGACTGTGGCCGCG 1020
DB |||||
961 GCTTGCAGATATCATGTTGGGAAATGGCCGCTTTTCTGGAATCATCGACTGTGGCCGCG 1020
QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCTGGCTACCGTGATATGCTGAAGAGC 1080
DB |||||
1021 TGGGTGTGCGGACCGCTATCAGGACATAGCTGGCTACCGTGATATGCTGAAGAGC 1080
QY 1081 TTGCGGCGAATGGGTGACCGCTTCTCGTGTGAGGATATCGCGCTCCCGATTCG 1140
DB |||||
1081 TTGCGGCGAATGGGTGACCGCTTCTCGTGTGAGGATATCGCGCTCCCGATTCG 1140
QY 1141 AGCGATCGCCTTCTATCGCCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
DB |||||
1141 AGCGATCGCCTTCTATCGCCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTAAGCTTACTGGC 1260
DB |||||
1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTAAGCTTACTGGC 1260
QY 1261 CGAAGCCGCTTGAATAAGGCGGTGCGTTTGTCTATATGTTTTCACCAATATTG 1320
DB |||||
1261 CGAAGCCGCTTGAATAAGGCGGTGCGTTTGTCTATATGTTTTCACCAATATTG 1320

QY 1321 CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT 1380
DB |||||
1321 CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT 1380
QY 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTGCTGAAGGAACA 1440
DB |||||
1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTGCTGAAGGAACA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGCGACCCCTTGTGAGGAGCGG 1500
DB |||||
1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGCGACCCCTTGTGAGGAGCGG 1500
QY 1501 AACCCCCACCTGCGGACAGGTGCTCTGCGGCCAAAGCCACCGTGTATAGATACACT 1560
DB |||||
1501 AACCCCCACCTGCGGACAGGTGCTCTGCGGCCAAAGCCACCGTGTATAGATACACT 1560
QY 1561 GCAAGGCGGACAAACCCAGTGCACGTTGTGAGTTGGATGAGTGTGGAAGAGTCAAA 1620
DB |||||
1561 GCAAGGCGGACAAACCCAGTGCACGTTGTGAGTTGGATGAGTGTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGTGAAGGATGCCAGAGGTTACCCCATGT 1680
DB |||||
1621 TGGCTCTCTCAAGCGTATTCAACAGGGGTGAAGGATGCCAGAGGTTACCCCATGT 1680
QY 1681 ATGGGATCTGATCTGCGGCTCGGTGCACATGCTTTTACATGTTTGTAGTCGAGGTTAAAA 1740
DB |||||
1681 ATGGGATCTGATCTGCGGCTCGGTGCACATGCTTTTACATGTTTGTAGTCGAGGTTAAAA 1740
QY 1741 AAGCTCTAGGCCCCCGAAACCAAGGGGACGTTGTTTCTTTGAAAAACGATATACC 1800
DB |||||
1741 AAGCTCTAGGCCCCCGAAACCAAGGGGACGTTGTTTCTTTGAAAAACGATATACC 1800
QY 1801 ATGGCGCTATTACGGCTTACTCCCAACACGAGGCGCTTCTGCTGCATCATCACT 1860
DB |||||
1801 ATGGCGCTATTACGGCTTACTCCCAACACGAGGCGCTTCTGCTGCATCATCACT 1860
QY 1861 AGCTCACAAGCGGACAGGAACCAAGGTGAGGGGAGGTCCAGGTGTCTCCACCGCA 1920
DB |||||
1861 AGCTCACAAGCGGACAGGAACCAAGGTGAGGGGAGGTCCAGGTGTCTCCACCGCA 1920
QY 1921 ACACATCTTCTGCGGACCTGCTCAATGCGGTGTGTTGGACTGCTATCATGTTGCC 1980
DB |||||
1921 ACACATCTTCTGCGGACCTGCTCAATGCGGTGTGTTGGACTGCTATCATGTTGCC 1980
QY 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCAGGAGGTTACCAATGTGGAC 2040
DB |||||
1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCAGGAGGTTACCAATGTGGAC 2040
QY 2041 CAGGACCTGCTGCGTGGCAAGGCCCCCGGGGCGGTTCTTGCACCATGCACTGC 2100
DB |||||
2041 CAGGACCTGCTGCGTGGCAAGGCCCCCGGGGCGGTTCTTGCACCATGCACTGC 2100
QY 2101 GCGAGCTGCGACCTTCTGCTGCGAGGATGCGGATGTCATTCGCGTGGCGGCGG 2160
DB |||||
2101 GCGAGCTGCGACCTTCTGCTGCGAGGATGCGGATGTCATTCGCGTGGCGGCGG 2160
QY 2161 GCGGACGAGGCGGAGCTTCTTCCCGCGGCGCTTCTGAGGAGGCTTTCG 2220
DB |||||
2161 GCGGACGAGGCGGAGCTTCTTCCCGCGGCGCTTCTGAGGAGGCTTTCG 2220
QY 2221 GCGGTCACCTGCTGCGGCGGACGCTGTGGGCTTCTTTCGCGGCTGCGGCTGTC 2280
DB |||||
2221 GCGGTCACCTGCTGCGGCGGACGCTGTGGGCTTCTTTCGCGGCTGCGGCTGTC 2280
QY 2281 ACCGAGGCGGTTGGAAGGCGGCTGGAATTTGTAACCGTGTGAGTCTATGGAACCACTATG 2340
DB |||||
2281 ACCGAGGCGGTTGGAAGGCGGCTGGAATTTGTAACCGTGTGAGTCTATGGAACCACTATG 2340
QY 2341 CCGTCCCGGCTTTCAGGACAACTCGTCCCTCCCGCGGCTACCGGACGATTCAGGTG 2400
DB |||||
2341 CCGTCCCGGCTTTCAGGACAACTCGTCCCTCCCGCGGCTACCGGACGATTCAGGTG 2400
QY 2401 GCCATCTACAGCCCCCTTCTGTTAGCGGCAAGAGACATAAGGTGCGGCTGCTGTGCA 2460

[illegible]

		7861	TTTTCTCCTTTTTTTTTTTCCTTTTCTTTTCCCTTTTCTTTTGGTGCTCCATCTTAGCGCCCTAGTCAACGCCG	7980
Db		7921	TAGCTGTGAAGGTCGGTGCAGCGCTTCGACTGCAGAGAGTCTCATACTATGGCCTCTCTCTGC	7980
Qy		7921	TAGCTGTGAAGGTCGGTGCAGCGCTTCGACTGCAGAGAGTCTCATACTATGGCCTCTCTCTGC	7980
Db		7921	TAGCTGTGAAGGTCGGTGCAGCGCTTCGACTGCAGAGAGTCTCATACTATGGCCTCTCTCTGC	7980
Qy		7981	AGATCAAGTACT 7992	
Db		7981	AGATCAAGTACT 7992	
		RESULT 6		
		ABK91448		
ID		ABK91448	standard; DNA; 10690 BP.	
XX		AC	ABK91448;	
XX		DT	15-NOV-2002 (first entry)	
XX		DE	Hepatitis C virus vector construct pHCVNeo.17ml5.	
XX		KW	HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;	
KW		KW	hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;	
KW		KW	internal ribosome entry site; IRES; NS5A; HCV replication; mutant.	
OS		OS	Hepatitis C virus.	
OS		OS	Encephalomyocarditis virus.	
OS		OS	Escherichia coli.	
OS		OS	Enterobacteria phage T7.	
XX		XX	Synthetic.	
FH		Key	Location/Qualifiers	
FT		5'UTR	1..341	
FT		/tag=	a	
FT		CDS	342..1181	
FT		/tag=	b	
FT		/product=	"Core-neo fusion protein"	
FT		/product=	1190..1800	
FT		/tag=	c	
FT		/label=	IRES	
FT		/note=	"Internal ribosome entry site from EMCV"	
FT		/tag=	d	
FT		/product=	"Polyprotein"	
FT		/note=	"Comprising NS3, NS4A, NS4B, NS5A and NS5B"	
FT		mutation	replace (5320,G)	
FT		/tag=	e	
FT		3'UTR	7759..7991	
FT		/tag=	f	
FT		misc_feature	7992..10690	
FT		/tag=	g	
FT		/note=	"Plasmid derived sequences"	
XX		WO200259321-A2.		
PN		01-AUG-2002.		
PD		16-JAN-2002; 2002MO-EP000526.		
XX		23-JAN-2001; 2001US-0263479P.		
PR		(RICE-) IST RICERHE BIOL MOLECOLARE ANGELETTI.		
XX		De Francesco R, Migliaccio G, Paonessa G;		
PI		WPI; 2002-599793/64.		
DR		New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV		
PT		NS5 encoding region, or encephalomyocarditis virus (EMCV) internal		
FT		ribosome entry site (IRES) region, useful in studying HCV replication and		
XX		expression.		
PS		Claim 16; Page: 69pp; English.		

xx

The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing the altered nucleic acids cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and HCV expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVneo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

Sequence 10690 BP; 2335 A; 3045 C; 2907 G; 2403 T; 0 U; 0 Other;

Query Match 99.9%; Score 7984; DB 6; Length 10690;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60
DB	1	GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60
QY	61	TCCTACGACGAGAAAGCGTCTAGCATGGCGTACTATGAGTGTCTGTGAGAGCTTCCG	120
DB	61	TCCTACGACGAGAAAGCGTCTAGCATGGCGTACTATGAGTGTCTGTGAGAGCTTCCG	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGAAATGCGAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGAAATGCGAG	180
QY	181	GACGACGGGTCTCTTTCTGGATCAACCCGCTCAATGCTCGAGATTGGGCGTGCCCC	240
DB	181	GACGACGGGTCTCTTTCTGGATCAACCCGCTCAATGCTCGAGATTGGGCGTGCCCC	240
QY	241	GCGAGACTGCTAGCCGAGTAGTCTGGTTCGCAAGAGCCCTTGTGTAATGCTGATAGG	300
DB	241	GCGAGACTGCTAGCCGAGTAGTCTGGTTCGCAAGAGCCCTTGTGTAATGCTGATAGG	300
QY	301	GTGCTTGGAGTGCCCGGGAGTCTCGTAGACCGTGCACATGACGACGAATCCTAAAC	360
DB	301	GTGCTTGGAGTGCCCGGGAGTCTCGTAGACCGTGCACATGACGACGAATCCTAAAC	360
QY	361	CTCAAGAAACCAAGGCGCGCATGATTGAAACAAGATGATGCAACGAGGTTCTC	420
DB	361	CTCAAGAAACCAAGGCGCGCATGATTGAAACAAGATGATGCAACGAGGTTCTC	420
QY	421	CGGCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAGACATCGGCTGT	480
DB	421	CGGCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAGACATCGGCTGT	480
QY	481	CTGATGCGCGGTGTTCGGCTGTCAAGCGAGGGGGCCGGTCTTTTGTTCAGACCG	540
DB	481	CTGATGCGCGGTGTTCGGCTGTCAAGCGAGGGGGCCGGTCTTTTGTTCAGACCG	540
QY	541	ACCTGTCCGGTCCCTGAATGAATGACGAGCAGCGCGGTATCGTGGCTGGCCA	600
DB	541	ACCTGTCCGGTCCCTGAATGAATGACGAGCAGCGCGGTATCGTGGCTGGCCA	600
QY	601	CGACGGGCGTCTCTTGGCGAGCTGTCTGAGCTGTCTACTGAAAGGGGAGGACTGGC	660
DB	601	CGACGGGCGTCTCTTGGCGAGCTGTCTGAGCTGTCTACTGAAAGGGGAGGACTGGC	660

QY	661	TGCTATTGGGCGAAGTGGCGGGCAGGATCTCTGTATCTCACTTGTCTCTGCGGAGA	720
DB	661	TGCTATTGGGCGAAGTGGCGGGCAGGATCTCTGTATCTCACTTGTCTCTGCGGAGA	720
QY	721	AAGTATCCATCATGCTGTATGCAATGCGGCGGCTGCATACGCTTATCCGGTACTCGC	780
DB	721	AAGTATCCATCATGCTGTATGCAATGCGGCGGCTGCATACGCTTATCCGGTACTCGC	780
QY	781	CATTTCGACCAACCAAGCAATCCATCTGAGCGAGCAGTACTCGATGAGAGCGGTTC	840
DB	781	CATTTCGACCAACCAAGCAATCCATCTGAGCGAGCAGTACTCGATGAGAGCGGTTC	840
QY	841	TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGCTCGCGCAGCCGAACTGTTTCG	900
DB	841	TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGCTCGCGCAGCCGAACTGTTTCG	900
QY	901	CCAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCTGTGACCCATGSCGATGCTT	960
DB	901	CCAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCTGTGACCCATGSCGATGCTT	960
QY	961	GCTTCCGGAATATCATGCTGGAAATGCGCGCTTTCTGGAATTCATCGACTGCGCGGC	1020
DB	961	GCTTCCGGAATATCATGCTGGAAATGCGCGCTTTCTGGAATTCATCGACTGCGCGGC	1020
QY	1021	TGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTCTGGAAGC	1080
DB	1021	TGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTCTGGAAGC	1080
QY	1081	TTGCGCGGGAATGGGCTGACCGCTTCTGTGCTTTACGGTATCGCGCTCCCGATTTCG	1140
DB	1081	TTGCGCGGGAATGGGCTGACCGCTTCTGTGCTTTACGGTATCGCGCTCCCGATTTCG	1140
QY	1141	AGCGCATCGCTTCTATCGCTTCTTACGAGTCTCTGAGTTTAAACAGACACCAAGC	1200
DB	1141	AGCGCATCGCTTCTATCGCTTCTTACGAGTCTCTGAGTTTAAACAGACACCAAGC	1200
QY	1201	GTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCGCTTACGTTTACTTGGC	1260
DB	1201	GTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCGCTTACGTTTACTTGGC	1260
QY	1261	CGAAGCGCTTGAATTAAGSCCGGTGCTTGTATATGTTATTTCCACCATATTG	1320
DB	1261	CGAAGCGCTTGAATTAAGSCCGGTGCTTGTATATGTTATTTCCACCATATTG	1320
QY	1321	CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGCGCTTCTTCTGACGAGATTCCT	1380
DB	1321	CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGCGCTTCTTCTGACGAGATTCCT	1380
QY	1381	AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGCTGTGAAGGAGCA	1440
DB	1381	AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGCTGTGAAGGAGCA	1440
QY	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTGTAGCGACCTTTGCGAGCGG	1500
DB	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTGTAGCGACCTTTGCGAGCGG	1500
QY	1501	AAACCCCGGCGGACAGGTGCTCTGCGGCGAAAGGACCGTGTATAGATACACCT	1560
DB	1501	AAACCCCGGCGGACAGGTGCTCTGCGGCGAAAGGACCGTGTATAGATACACCT	1560
QY	1561	GCAAGGCGGCAAAACCCAGTGCCTCTGCGGCGAAAGGACCGTGTATAGATACACCT	1620
DB	1561	GCAAGGCGGCAAAACCCAGTGCCTCTGCGGCGAAAGGACCGTGTATAGATACACCT	1620
QY	1621	TGGCTCTCTCAAGGCTATTCAAAGGGGCTGAAGGATGCCCAGAGGTACCCATTGT	1680
DB	1621	TGGCTCTCTCAAGGCTATTCAAAGGGGCTGAAGGATGCCCAGAGGTACCCATTGT	1680
QY	1681	ATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTATGTTTGTGAGGTTTAAA	1740
DB	1681	ATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTATGTTTGTGAGGTTTAAA	1740

Qy	1741	AACGCTCTAGCGCCCGGAAACCAAGGAGCGTGGTTTCTTGGAAACAGTAATACC	1800	Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACATC	2880
Db	1741	AACGCTCTAGCGCCCGGAAACCAAGGAGCGTGGTTTCTTGGAAACAGTAATACC	1800	Qy	2881	AAGGGGGAGGACACCTCTATTTCTGCAATCCAAAGAAATGTGTATGAGCTCGCGCG	2940
Qy	1801	ATGGCGCTATTACGGCTTACTCCCAACAGACGCGAGCTTACTTGGCTGCATCACT	1860	Db	2881	AAGGGGGAGGACACCTCTATTTCTGCAATCCAAAGAAATGTGTATGAGCTCGCGCG	2940
Db	1801	ATGGCGCTATTACGGCTTACTCCCAACAGACGCGAGCTTACTTGGCTGCATCACT	1860	Qy	2941	AAGCTGTCCGGCTCGGACTCAATGTGTAGCAATATTTACCGGGCCCTTGATTCGGTC	3000
Qy	1861	AGCTCTACAGCGCGGACAGGAACAGGTCCAGGGGAGGTCCAGGTGGTCTCCACGCA	1920	Db	2941	AAGCTGTCCGGCTCGGACTCAATGTGTAGCAATATTTACCGGGCCCTTGATTCGGTC	3000
Db	1861	AGCTCTACAGCGCGGACAGGAACAGGTCCAGGGGAGGTCCAGGTGGTCTCCACGCA	1920	Qy	3001	ATACCAACTAGCGAGACGTCATTTGTGTAGCAACGAGCGCTCTAATGACGGCTTTACC	3060
Qy	1921	ACACAATCTTTCTGGGACCTCGGTCAATGGCGTGTGTGGACTGTCTATCATGGTGCC	1980	Db	3001	ATACCAACTAGCGAGACGTCATTTGTGTAGCAACGAGCGCTCTAATGACGGCTTTACC	3060
Db	1921	ACACAATCTTTCTGGGACCTCGGTCAATGGCGTGTGTGGACTGTCTATCATGGTGCC	1980	Qy	3061	GGCGATTTCCGACTCAGTGTATCGACTGCAATATGTGTACCCACAGACAGTGTTCAGC	3120
Qy	1981	GGCTCAAGACCTTTGCGGCGCCAAAGGGCCCAATCACCAAAATGTACCAAAATGTGGAC	2040	Db	3061	GGCGATTTCCGACTCAGTGTATCGACTGCAATATGTGTACCCACAGACAGTGTTCAGC	3120
Db	1981	GGCTCAAGACCTTTGCGGCGCCAAAGGGCCCAATCACCAAAATGTACCAAAATGTGGAC	2040	Qy	3121	CTGGACCCGACCTTACCATTGAGACGACCGTGGCCACAGACGCGGTGTACGCTCG	3180
Qy	2041	CAGGACCTCGTGGTGAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGTC	2100	Db	3121	CTGGACCCGACCTTACCATTGAGACGACCGTGGCCACAGACGCGGTGTACGCTCG	3180
Db	2041	CAGGACCTCGTGGTGAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGTC	2100	Qy	3181	CAGCGGCGAGGAGGACGTCATTTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCAGGA	3240
Qy	2101	GGCAGCTCGGACCTTTTACTTGGTCAAGGAGGATGCGGATGTCATTTCCGGTGGCGGCGG	2160	Db	3181	CAGCGGCGAGGAGGACGTCATTTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCAGGA	3240
Db	2101	GGCAGCTCGGACCTTTTACTTGGTCAAGGAGGATGCGGATGTCATTTCCGGTGGCGGCGG	2160	Qy	3241	GAAACGCGCTCGGGCATGTTCCGATTTCTGCGAGTGTATGACGCGGGCTGT	3300
Qy	2161	GGGACAGGAGGGGAGCTACTCTCCCGGCGCGCTCTCTCTTGAAGGGCTCTTGG	2220	Db	3241	GAAACGCGCTCGGGCATGTTCCGATTTCTGCGAGTGTATGACGCGGGCTGT	3300
Db	2161	GGGACAGGAGGGGAGCTACTCTCCCGGCGCGCTCTCTCTTGAAGGGCTCTTGG	2220	Qy	3301	GCTTGTGTAGGCTCACGCGCCCGAGACCTCAGTTAGTGTGCGGGCTTACCTAAACACA	3360
Qy	2221	GGCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCATTTTTCGGGCTCGGCTGTC	2280	Db	3301	GCTTGTGTAGGCTCACGCGCCCGAGACCTCAGTTAGTGTGCGGGCTTACCTAAACACA	3360
Db	2221	GGCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCATTTTTCGGGCTCGGCTGTC	2280	Qy	3361	CAGGGTTGCCGTCTGCCAGGACCATCTGGAGTTCTGGGAGGCGTCTTTACAGGCTTC	3420
Qy	2281	ACCCGAGGGGTTGCGAAGCGGTGAGCTTTGTACCGGTGAGTCTATGGAACCACTATG	2340	Db	3361	CAGGGTTGCCGTCTGCCAGGACCATCTGGAGTTCTGGGAGGCGTCTTTACAGGCTTC	3420
Db	2281	ACCCGAGGGGTTGCGAAGCGGTGAGCTTTGTACCGGTGAGTCTATGGAACCACTATG	2340	Qy	3421	ACCCACATAGAGCCCATTTCTTCCAGACTTAAGACGAGGAGGAGCAACTTCCCTTAC	3480
Qy	2341	CGGTCCCGGCTTTACAGGACAACTCGTCCCTTCGGCGGTACCGCAGACATTCAGGTG	2400	Db	3421	ACCCACATAGAGCCCATTTCTTCCAGACTTAAGACGAGGAGGAGCAACTTCCCTTAC	3480
Db	2341	CGGTCCCGGCTTTACAGGACAACTCGTCCCTTCGGCGGTACCGCAGACATTCAGGTG	2400	Qy	3481	CTGGTAGCATACAGGCTACGGTGTGCGGACGAGGCTCAGGCTCCACTCCATCGTGGAC	3540
Qy	2401	GCCCATCTACAGCCCTTACTGTGTAGCGGCAAGACACTAAGGTGCGGCTGCGTATGCA	2460	Db	3481	CTGGTAGCATACAGGCTACGGTGTGCGGACGAGGCTCAGGCTCCACTCCATCGTGGAC	3540
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Qy	2461	GCCAAAGGGTATAAGGTGCTTGTCTGAACCCGTCGGTCCGCGCAACCTTAGGTTTCGGG	2520	Db	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCCTACGCTGCACGGGCAACGCGCCCTGCTG	3600
Db	2461	GCCAAAGGGTATAAGGTGCTTGTCTGAACCCGTCGGTCCGCGCAACCTTAGGTTTCGGG	2520	Qy	3601	TATAGGCTGGAGCGGTTCAAAACAGAGTTTACTACACACACCCCATTAACCAATATCATC	3660
Qy	2521	GGGTATATGCTTAAGGCACATGTGTATCGACCTTAAATCAGAACCGGGTAAAGACCATC	2580	Db	3601	TATAGGCTGGAGCGGTTCAAAACAGAGTTTACTACACACACCCCATTAACCAATATCATC	3660
Db	2521	GGGTATATGCTTAAGGCACATGTGTATCGACCTTAAATCAGAACCGGGTAAAGACCATC	2580	Qy	3661	ATGGCATGCAATGTGCGTGAACCTGGAGGTCGTCACGAGGACCTGGGTGCTGGTAGGGGA	3720
Qy	2581	ACCAAGGGTGGCCCGCATCAGCTACTCACCTATGGAAGTTTCTTTCGCGAGCGTGGTTC	2640	Db	3661	ATGGCATGCAATGTGCGTGAACCTGGAGGTCGTCACGAGGACCTGGGTGCTGGTAGGGGA	3720
Db	2581	ACCAAGGGTGGCCCGCATCAGCTACTCACCTATGGAAGTTTCTTTCGCGAGCGTGGTTC	2640	Qy	3721	GTCTTAGCAGCTCTGGCGGTTATTCCTGCACACAGGAGCGTGGTTCATTTGTGGGCGG	3780
Qy	2641	TCGTGGGGCGCTTATGACATCAATATGTGTAGTGCCACTCAACTGACTCGACCACT	2700	Db	3721	GTCTTAGCAGCTCTGGCGGTTATTCCTGCACACAGGAGCGTGGTTCATTTGTGGGCGG	3780
Db	2641	TCGTGGGGCGCTTATGACATCAATATGTGTAGTGCCACTCAACTGACTCGACCACT	2700	Qy	3781	ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Qy	2701	ATCTGGGACATCGGACAGTCTTGGAACCAAGCGGAGACGGTGGAGCGGACTCGTGGT	2760	Db	3781	ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Db	2701	ATCTGGGACATCGGACAGTCTTGGAACCAAGCGGAGACGGTGGAGCGGACTCGTGGT	2760	Qy	3841	GATGAGATGGAAGTGGCGCTCACCTCTCCCTTACATCGAAGGGAATGACGCTGCC	3900
Qy	2761	CTCGCCACCGCTACGCTTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGTG	2820	Db	3841	GATGAGATGGAAGTGGCGCTCACCTCTCCCTTACATCGAAGGGAATGACGCTGCC	3900
Db	2761	CTCGCCACCGCTACGCTTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGTG	2820	Qy	3901	GAAACAATCAACAGAGGCAATCGGTTTGTGCAAAACAGCCACCAAGAGCGGAGCT	3960
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACATC	2880				

QY	6121	CTGCGGAGAGAGGTCACTTTGACAGACTGCGGTCTGTGAGGACCACTACCGGGAC	6180	Db	7201	TCCTGGCTAGGCAACATCATGTATGCGCCCACTTGTGGGCAAGGATGATCCTGATG	7260
Db	6121	CTGCGGAGAGAGGTCACTTTGACAGACTGCGGTCTGTGAGGACCACTACCGGGAC	6180	QY	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAAAAGCCCTAGATTGTTCAG	7320
QY	6181	GTGCTCAAGGAGATGAAGGCGAAGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAG	6240	Db	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAAAAGCCCTAGATTGTTCAG	7320
Db	6181	GTGCTCAAGGAGATGAAGGCGAAGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAG	6240	QY	7321	ATCTACGGGGGCTGTACTTCCATTTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC	7380
QY	6241	GAAGCCTGTAAAGCTGAAGCCGCCCACTTTCGGCCAGATCTAAATTTGGCTATGGGGCAAG	6300	Db	7321	ATCTACGGGGGCTGTACTTCCATTTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC	7380
Db	6241	GAAGCCTGTAAAGCTGAAGCCGCCCACTTTCGGCCAGATCTAAATTTGGCTATGGGGCAAG	6300	QY	7381	CATGCGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
QY	6301	GACGTCGGGAACCTATCCAGCAAGCGCTTAAACCACTCCGCTCCGTTGGAAGGACTTG	6360	Db	7381	CATGCGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Db	6301	GACGTCGGGAACCTATCCAGCAAGCGCTTAAACCACTCCGCTCCGTTGGAAGGACTTG	6360	QY	7441	TCATGCTCCCTCAGGAACCTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT	7500
QY	6361	CTGGAAGACACTGAGACACCAATTCACACCACTCATGCGCAAAATGAGGTTTCTGTC	6420	Db	7441	TCATGCTCCCTCAGGAACCTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT	7500
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QY	6421	GTCCCAACAGAGAGGGGGCGCGAAGCGAGTCCGCTTATCGTATTTCCAGATTGGGG	6480	Db	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGAGGGTGCACCTTGTGGCAAGTACCTCTTC	7560
Db	6421	GTCCCAACAGAGAGGGGGCGCGAAGCGAGTCCGCTTATCGTATTTCCAGATTGGGG	6480	QY	7561	AACCTGGGAGTTAAGAACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCCGATTGGAT	7620
QY	6481	GTTCGCTGTGCGAGAAATGCGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG	6540	Db	7561	AACCTGGGAGTTAAGAACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCCGATTGGAT	7620
Db	6481	GTTCGCTGTGCGAGAAATGCGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG	6540	QY	7621	TTATCCAGCTGGTTCGTTGCTGTTACAGCGGGGAGACATATATCAGAGCCTGTCTCGT	7680
QY	6541	ATGGGCTCTTCATACGGAATTCCTCTGACAGCGGTGAGTTCCTGTGTAAT	6600	Db	7621	TTATCCAGCTGGTTCGTTGCTGTTACAGCGGGGAGACATATATCAGAGCCTGTCTCGT	7680
Db	6541	ATGGGCTCTTCATACGGAATTCCTCTGACAGCGGTGAGTTCCTGTGTAAT	6600	QY	7681	GCCGACCCCGCTGGTTCATGTGGTCCCTACTCTTCTTGTAGGGTAGGCATCTAT	7740
QY	6601	GCTTGAAGCGAAGAAATGCCCTATGCGCTTTCGATATGACACCCCGCTTGTGACTCA	6660	Db	7681	GCCGACCCCGCTGGTTCATGTGGTCCCTACTCTTCTTGTAGGGTAGGCATCTAT	7740
Db	6601	GCTTGAAGCGAAGAAATGCCCTATGCGCTTTCGATATGACACCCCGCTTGTGACTCA	6660	QY	7741	CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCCAATAGGCCATCTCTTTT	7800
QY	6661	ACGGTCACTGAGAAATGCGCTTTCGATATGACACCCCGCTTGTGACTCA	6720	Db	7741	CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCCAATAGGCCATCTCTTTT	7800
Db	6661	ACGGTCACTGAGAAATGCGCTTTCGATATGACACCCCGCTTGTGACTCA	6720	QY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
QY	6721	CCGGAAGCCAGACAGGCCATAGGTCCTCACAGAGCGGCTTTACATCGGGGGCCCGCTG	6780	Db	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	6721	CCGGAAGCCAGACAGGCCATAGGTCCTCACAGAGCGGCTTTACATCGGGGGCCCGCTG	6780	QY	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
QY	6781	ACTAATTTCTAAAGGCGAGAACTGCGGCTATCGCGCTGCGCGCGCGCGCTGTACTGAGC	6840	Db	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	6781	ACTAATTTCTAAAGGCGAGAACTGCGGCTATCGCGCTGCGCGCGCGCGCTGTACTGAGC	6840	QY	7921	TAGCTGTGAAAGGTCCGTTGAGCGGCTTGAATCTGAGAGAGTGTGATCTAGGCTCTCTGC	7980
QY	6841	ACCAGCTGCGGTAAATACCTTCACTGTTACTTGAAGCGCGCTGCGCGCTGCGAGCTGCG	6900	Db	7921	TAGCTGTGAAAGGTCCGTTGAGCGGCTTGAATCTGAGAGAGTGTGATCTAGGCTCTCTGC	7980
Db	6841	ACCAGCTGCGGTAAATACCTTCACTGTTACTTGAAGCGCGCTGCGCGCTGCGAGCTGCG	6900	QY	7981	AGATCAAGTACT 7992	
QY	6901	AAAGCTCAGGACTGACAGGAGCGAGGAGGCTTACGAGGCGCTGCGCGCTGCGAGCTGCG	6960	Db	7981	AGATCAAGTACT 7992	
Db	6901	AAAGCTCAGGACTGACAGGAGCGAGGAGGCTTACGAGGCGCTGCGCGCTGCGAGCTGCG	6960				
QY	6961	GCGGGAGCCCAAGAGGAGCGAGGAGGCTTACGAGGCGCTTACGAGGCGCTTACGAGTAC	7020				
Db	6961	GCGGGAGCCCAAGAGGAGCGAGGAGGCTTACGAGGCGCTTACGAGGCGCTTACGAGTAC	7020				
QY	7021	TCTGCCCCCTTGGGAGCCCGCCCAACACCAAGATACGACTTGGAGTTGATAACATCATGC	7080				
Db	7021	TCTGCCCCCTTGGGAGCCCGCCCAACACCAAGATACGACTTGGAGTTGATAACATCATGC	7080				
QY	7081	TCCTTCCCAATGTGTCAGTCCGCGCAGATGTCATCTGGCAAAAGGGTGTACTATCTACCCGT	7140				
Db	7081	TCCTTCCCAATGTGTCAGTCCGCGCAGATGTCATCTGGCAAAAGGGTGTACTATCTACCCGT	7140				
QY	7141	GACCCCAACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200				
Db	7141	GACCCCAACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200				
QY	7201	TCCTGGCTAGGCAACATCATGTATGCGGCCCACTTGTGGGCAAGGATGATCCTGATG	7260				

RESULT 7
 ABK91435
 ID ABK91435 standard; DNA; 10690 BP.
 XX
 AC ABK91435;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Hepatitis C virus vector construct pHCVNeo.17m2.
 XX
 KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
 KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
 KW internal ribosome entry site; IRES; NSSA; HCV replication; mutant.
 OS Hepatitis C virus.
 OS Encephalomyocarditis virus.
 OS Escherichia coli.

OS Enterobacteria phage T7.
 XX Synthetic.
 XX Key Location/Qualifiers
 PH 5'UTR 1..341
 FT /*tag= a
 FT CDS 342..1181
 FT /*tag= b
 FT misc_signal /product= "Core-neo fusion protein"
 FT 1190..1800
 FT /*tag= c
 FT /label= IRES
 FT /note= "Internal ribosome entry site from EMCV"
 FT CDS 1801..7758
 FT /*tag= d
 FT /product= "Polyprotein"
 FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
 FT mutation replace(5243,C)
 FT /*tag= e
 FT 3'UTR 7759..7991
 FT /*tag= f
 FT misc_feature 7992..10690
 FT /*tag= g
 FT /note= "Plasmid derived sequences"
 XX
 PN WO200259321-A2.
 XX
 XX 01-AUG-2002.
 XX
 XX 16-JAN-2002; 2002WO-EP000526.
 PF
 XX
 XX 23-JAN-2001; 2001US-0263479P.
 PR
 XX
 XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
 PA
 PI De Francesco R, Migliaccio G, Paonessa G;
 XX
 XX WPI; 2002-599793/64.
 XX
 PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
 PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
 PT ribosome entry site (IRES) region, useful in studying HCV replication and
 PT expression.
 XX
 PS Claim 16; Page; 69pp; English.
 XX
 CC The invention relates to nucleic acid molecules comprising altered HCV
 CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
 CC internal ribosome entry site (IRES) region coding for one or more NS3,
 CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
 CC are detailed in the specification. Also included are (1) an expression
 CC vector comprising a nucleotide sequence coding for the altered nucleic
 CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
 CC recombinant cell human hepatoma cell comprising the altered nucleic acids
 CC ; (3) a recombinant cell produced by introducing into a human hepatoma
 CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
 CC replicon enhanced cell or which containing a functional HCV replicon; (5)
 CC an HCV replicon enhanced cells made in the method; and (6) measuring the
 CC ability of a compound to affect HCV activity. The HCV replicons and HCV
 CC replicon enhanced cells are useful in studying HCV replication and
 CC expression, and HCV and host cell interactions, producing HCV RNA and
 CC proteins, and providing a system for measuring the ability of a compound
 CC to modulate one or more HCV activities e.g. to discover drugs which may
 CC treat HCV mediated diseases such as liver failure, cirrhosis and
 CC hepatocellular carcinoma. The present sequence is an HCV based vector
 CC pHCVneo.17 mutant of the invention. Note: The present sequence is not
 CC shown in the specification but was created by the indexer using the HCV
 CC vector sequence appearing as ABR91412 and the information in Claim 16
 XX
 SQ Sequence 10690 BP; 2334 A; 3044 C; 2908 G; 2404 T; 0 U; 0 Other;

Query Match

Best Local Similarity 99.9%; Score 7984; DB 6; Length 10690;

Pred. No. 0;

		Matches 7987;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
QY	1	GCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGAACTACTG	60							
DB	1	GCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGAACTACTG	60							
QY	61	TCATTACGACAGAAACGCTCTAGCCATGGCGTTAGTATGAGTGTGTCGAGCTCCAGAAC	120							
DB	61	TCATTACGACAGAAACGCTCTAGCCATGGCGTTAGTATGAGTGTGTCGAGCTCCAGAAC	120							
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGGGAACCGGTGAGTACACCGGAATTCGAG	180							
DB	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGGGAACCGGTGAGTACACCGGAATTCGAG	180							
QY	181	GACGACCGGTCCTTTCTTGGATCAAGCCCGTCAATGCTCAATGCTGGAGATTGGCGTGC	240							
DB	181	GACGACCGGTCCTTTCTTGGATCAAGCCCGTCAATGCTGGAGATTGGCGTGC	240							
QY	241	GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGCCCTTGTGTTACTGCTGATAGG	300							
DB	241	GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGCCCTTGTGTTACTGCTGATAGG	300							
QY	301	GTGCTTCGAGTGCCTCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGATCCTTAAC	360							
DB	301	GTGCTTCGAGTGCCTCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGATCCTTAAC	360							
QY	361	CTCAAGAAAAAACAAGGCGGCCATGATTGAACAAGATGGATTGCAAGAGTTCTC	420							
DB	361	CTCAAGAAAAAACAAGGCGGCCATGATTGAACAAGATGGATTGCAAGAGTTCTC	420							
QY	421	CGGCGCTTGGTGGAGAGCTATTGGCTATGATGGGCAACAAGATCGGTGCT	480							
DB	421	CGGCGCTTGGTGGAGAGCTATTGGCTATGATGGGCAACAAGATCGGTGCT	480							
QY	481	CTGATGCGCGCTTCCCGGCTGTCAGCGCAGGCGCGCGCTCTTTTGTCAAGACCG	540							
DB	481	CTGATGCGCGCTTCCCGGCTGTCAGCGCAGGCGCGCGCTCTTTTGTCAAGACCG	540							
QY	541	ACTGTCCGTCCTGTAATGAACTGCAGACAGGCGCGGCTATCTGGTGGCCCA	600							
DB	541	ACTGTCCGTCCTGTAATGAACTGCAGACAGGCGCGGCTATCTGGTGGCCCA	600							
QY	601	CGACGGCGTTCCTGCGAGCTGTGTCAGCTGTAAGCGGGAAGGAGCTGGC	660							
DB	601	CGACGGCGTTCCTGCGAGCTGTGTCAGCTGTAAGCGGGAAGGAGCTGGC	660							
QY	661	TGCTATTGGCGAGTGCAGGCGAGATCTCTGTCATCTCACTTGTCTTCTGCGGAGA	720							
DB	661	TGCTATTGGCGAGTGCAGGCGAGATCTCTGTCATCTCACTTGTCTTCTGCGGAGA	720							
QY	721	AAGTATCCATCATGCTGATGCAATCGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780							
DB	721	AAGTATCCATCATGCTGATGCAATCGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780							
QY	781	CATTGACCAACAGGAAACATCGATCGAGGAGCAGTACTCGATGGAAGCGCGTC	840							
DB	781	CATTGACCAACAGGAAACATCGATCGAGGAGCAGTACTCGATGGAAGCGCGTC	840							
QY	841	TTGTCGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGGCCAGCGACTTTTCG	900							
DB	841	TTGTCGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGGCCAGCGACTTTTCG	900							
QY	901	CCAGGCTCAAGCGCGCATGTCGCCGAGGATCTGTCGTGACCCATGGCGATGCTC	960							
DB	901	CCAGGCTCAAGCGCGCATGTCGCCGAGGATCTGTCGTGACCCATGGCGATGCTC	960							
QY	961	GCTTCCGAAATCATGTTGGAAATGCGCGCTTTTCTGGATTTCATCGACTGTGCGCGC	1020							
DB	961	GCTTCCGAAATCATGTTGGAAATGCGCGCTTTTCTGGATTTCATCGACTGTGCGCGC	1020							
QY	1021	TGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGCTGATATTGCTGAAGAGC	1080							
DB	1021	TGGGTGTGCGGACCGCTATCAGGACATAGCTTGGCTACCGCTGATATTGCTGAAGAGC	1080							

QY 1081 TTGGCGGGAATGGGCTGAACGGCTTCCTGCTGCTTTTACGGTATCGCGCTCCCGATTGCG 1140
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QY 1141 AGCGATCGCCTTCTATCGCCTTCTTGACGAGTCTCTGAGTTTAAACAGACACACACG 1200
DB 1141 AGCGATCGCCTTCTATCGCCTTCTTGACGAGTCTCTGAGTTTAAACAGACACACACG 1200
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DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTACTGCG 1260
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DB 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTTCTGACGAGCATCT 1380
QY 1381 AGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTGAAGGA 1440
DB 1381 AGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTGAAGGA 1440
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DB 1441 GTTCTCTGGAAGCTTCTGGAAGCAAAACAAAGTCTGTGAGGAGTCTGTTGAATGTCTGTGAAGGAG 1500
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DB 1621 TGGCTCTCTAAGGCTATTCACAAAGGCGCTGAGGATGCGGAGGAGTACCCCATCT 1680
QY 1681 ATGGGATCTGATCTGGGCTCGGTGCACATGTTTACATGTTTGTAGTCTGAGGTTAA 1740
DB 1681 ATGGGATCTGATCTGGGCTCGGTGCACATGTTTACATGTTTGTAGTCTGAGGTTAA 1740
QY 1741 AAGCTCTAGGCGCCCGAACCAACCGGAGCGTGGTTTCTTTGAAAACACGATATACC 1800
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QY 2161 GGCAGACAGGCGGAGCCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAGGCTCTTCG 2220
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DB 3121 CTGAGCCCGGACCTTACCATTTGAGACGACCGTGCACAAAGACGCGGTGTCACGCTCG 3180
QY 3181 CAGCGGCGAGGAGGACTGTTAGGGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 3240
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Db 7981 AGATCAAGTACT 7992

RESULT 8
ABK91243
ID ABK91243 standard; DNA; 10690 BP.
XX AC ABK91243;
XX DT 15-NOV-2002 (first entry)
XX DE Hepatitis C virus vector construct pHCVNeo.17.m1.
XX KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

XX Key Location/Qualifiers
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FT /*tag= f
FT misc_feature 7992..10690
FT /*tag= g
FT /note= "Plasmid derived sequences"
XX WO200259321-A2.
XX 01-AUG-2002.
PD

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XX 16-JAN-2002; 2002WO-EP000526.
PF 23-JAN-2001; 2001US-0263479P.
XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX WPI; 2002-599793/64.
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX Example 1; Page; 69pp; English.
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX ; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is an HCV based vector
XX pHCVNeo.17 mutant of the invention. Note: The present sequence is not
XX shown in the specification but was created by the indexer using the HCV
XX vector sequence appearing as ABK91412 and the information in example 1
XX SQ Sequence 10690 BP; 2333 A; 3046 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 99.9%; Score 7984; DB 6; Length 10690;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 121 CCCCCCTCCCGGAGAGCCATAGTGTGTCGGAACCGGTGAGTACACCGGAATTCGCGAG 180
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Qy 841 TTGTCGATCAGGATGATCTGAGCAAGAGATCAGGGGCTCGCGAGCGAAGCTGTTTCG 900
Db 841 TTGTCGATCAGGATGATCTGAGCAAGAGATCAGGGGCTCGCGAGCGAAGCTGTTTCG 900
Qy 901 CCAGGCTCAAGCGCGCATGCGCGAGGAGATCTCGTGTGATGCCATGCGAGTGCCT 960
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RESULT 9
ABK91434
ID ABK91434 standard; DNA; 10690 BP.
XX
AC ABK91434;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus vector construct pHCVNeo.17m0.
XX
KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX
OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.
XX
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FT /*tag= f
FT misc_feature 7992..10690
FT /*tag= g
FT /*note= "Plasmid derived sequences"
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XX
PD 01-AUG-2002.
XX
PF 16-JAN-2002; 2002WO-EP000526.
XX
PR 23-JAN-2001; 2001US-0263479P.
XX
PA (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
XX
PI De Francesco R, Migliaccio G, Paonessa G;
XX
DR WPI; 2002-599793/64.
XX
PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
PS Claim 16; Page; 69pp; English.
XX
CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
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CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHCVneo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in Claim 16
XX
SQ Sequence 10690 BP; 2335 A; 3044 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 99.9%; Score 7984; DB 6; Length 10690;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 421 CGGCGCTTGGTGGAGGCTATTCGGCTATGACTGGGCAACACAGACAAATCGGCTGCT 480

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DB 781 CATTCGACCAACAAGCGAAACATCGATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
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DB 841 TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCG 900
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QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTCGCTACCCGCTGATATTCGTGAAGAC 1080
DB 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTCGCTACCCGCTGATATTCGTGAAGAC 1080
QY 1081 TTGCGCGGAATGGGCTGACCGCTTCTCGTGTGCTTACGATATCGCGCTCCCGATTCCG 1140
DB 1081 TTGCGCGGAATGGGCTGACCGCTTCTCGTGTGCTTACGATATCGCGCTCCCGATTCCG 1140
QY 1141 AGCGCATCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
DB 1141 AGCGCATCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTAACCTTACTGCG 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTAACCTTACTGCG 1260
QY 1261 CGAAGCGCTTGGAAATGAGCGGCTGTGCTTGTCTATATGTTATTTTCCACCATATTG 1320
DB 1261 CGAAGCGCTTGGAAATGAGCGGCTGTGCTTGTCTATATGTTATTTTCCACCATATTG 1320
QY 1321 CGGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTTGTGAGGACATTCCT 1380
DB 1321 CGGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTTGTGAGGACATTCCT 1380
QY 1381 AGGGGTCTTTTCCCTCTCGCAAGGAATGCAAGGTCTGTGAAATGTCGTGAAGGAGCA 1440
DB 1381 AGGGGTCTTTTCCCTCTCGCAAGGAATGCAAGGTCTGTGAAATGTCGTGAAGGAGCA 1440
QY 1441 GTTCTCTGGAAGCTTTTGAAGACAAAACAACCTGTGTAGGACCTTTTTCAGGACGCG 1500
DB 1441 GTTCTCTGGAAGCTTTTGAAGACAAAACAACCTGTGTAGGACCTTTTTCAGGACGCG 1500
QY 1501 AACCCCGACCTGCGGACAGGTGCTGCGGCAAAAGCCACGTGTATGAAGATACACCT 1560
DB 1501 AACCCCGACCTGCGGACAGGTGCTGCGGCAAAAGCCACGTGTATGAAGATACACCT 1560
QY 1561 GCAAGGCGGCAAAACCCAGTCCACGTTGTGAGTTGGAATGTTGGAAGAGTCAAA 1620
DB 1561 GCAAGGCGGCAAAACCCAGTCCACGTTGTGAGTTGGAATGTTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCACAGAGGCTGAAAGATGCGGAGGTTACCCCATGT 1680
DB 1621 TGGCTCTCTCAAGCGTATTCACAGAGGCTGAAAGATGCGGAGGTTACCCCATGT 1680
QY 1681 ATGGGATCTCATCTGGGGCTCGGTGCACATGCTTTTACATGTTTGTAGTGAAGTTAAA 1740
DB 1681 ATGGGATCTCATCTGGGGCTCGGTGCACATGCTTTTACATGTTTGTAGTGAAGTTAAA 1740
QY 1741 AAGCTCTAGGCGCCCGGCAACACAGGAGCGTGGTTCCTTTGAAACACGATATAC 1800
DB 1741 AAGCTCTAGGCGCCCGGCAACACAGGAGCGTGGTTCCTTTGAAACACGATATAC 1800
QY 1801 ATGGCGCTTATTCAGGCTTACTCCCAACAGCGAGGCTTCTTGGCTGCTCATCACT 1860
DB 1801 ATGGCGCTTATTCAGGCTTACTCCCAACAGCGAGGCTTCTTGGCTGCTCATCACT 1860
QY 1861 AGCCTCACAGCGCGGACAGGAACAGGTGAGGGGAGGTCCAGGTGGTCTCCACCGCA 1920
DB 1861 AGCCTCACAGCGCGGACAGGAACAGGTGAGGGGAGGTCCAGGTGGTCTCCACCGCA 1920

QY	1921	ACACAACTTTCTTCTGCGACCTGCTGCTCAATGCGGTGTGTGGACTGTCTATCATGTGCG	1980
Db	1921	ACACAACTTTCTTCTGCGACCTGCGTCAATGCGGTGTGTGGACTGTCTATCATGTGCG	1980
QY	1981	GGCTCAAAAGACCTTTCGCGGCCCAAGGCGCCCAATCACCCAAATGATACCAATGTGGAC	2040
Db	1981	GGCTCAAAAGACCTTTCGCGGCCCAAGGCGCCCAATCACCCAAATGATACCAATGTGGAC	2040
QY	2041	CAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGCGTTCCTTGACACCATGCACTTGC	2100
Db	2041	CAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGCGTTCCTTGACACCATGCACTTGC	2100
QY	2101	GGCAGCTCGGACCTTTACTTGTGTACGAGGCATGCGATGTCAATTCGCGTGGCGGGG	2160
Db	2101	GGCAGCTCGGACCTTTACTTGTGTACGAGGCATGCGATGTCAATTCGCGTGGCGGGG	2160
QY	2161	GGCGACAGAGGGGAGCCCTACTCTCCCGCCAGCGCGCTCTCTACTTGAAGGGCTCTTCG	2220
Db	2161	GGCGACAGAGGGGAGCCCTACTCTCCCGCCAGCGCGCTCTCTACTTGAAGGGCTCTTCG	2220
QY	2221	GGCGGTCCACTGCTCTGCCCTTCGCGGACGCTGTGGGCATCTTTCGCGCTGCGGTGTC	2280
Db	2221	GGCGGTCCACTGCTCTGCCCTTCGCGGACGCTGTGGGCATCTTTCGCGCTGCGGTGTC	2280
QY	2281	ACCGAGGGGTTGCGAAGCGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
Db	2281	ACCGAGGGGTTGCGAAGCGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
QY	2341	CGGTCCCGGCTTTCACGCAACACTGCTGCCCTCCCGCGGTACCGCAGACATTCAGGTG	2400
Db	2341	CGGTCCCGGCTTTCACGCAACACTGCTGCCCTCCCGCGGTACCGCAGACATTCAGGTG	2400
QY	2401	GCCCATCTACACGCGCTTACTGTTAGCGGCAAGAGCACTAAGGTGCGCGCTGCGTATGCA	2460
Db	2401	GCCCATCTACACGCGCTTACTGTTAGCGGCAAGAGCACTAAGGTGCGCGCTGCGTATGCA	2460
QY	2461	GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGGTGCGCGCCACCTAGGTTCGGG	2520
Db	2461	GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGGTGCGCGCCACCTAGGTTCGGG	2520
QY	2521	GCCTATATGCTAAGGCACTGTTATGCAACCTTAACATGAGACCGGGGTAAAGACCATC	2580
Db	2521	GCCTATATGCTAAGGCACTGTTATGCAACCTTAACATGAGACCGGGGTAAAGACCATC	2580
QY	2581	ACCAAGGTTGCGCCCATCAGCTTACTCCACCTATGCAAGTTCTTTCGCGAGCTGCTGTC	2640
Db	2581	ACCAAGGTTGCGCCCATCAGCTTACTCCACCTATGCAAGTTCTTTCGCGAGCTGCTGTC	2640
QY	2641	TCTGGGGCGCTATGACATCAATATGTGATGAGTGCCACTCAACTGACTCGACCACT	2700
Db	2641	TCTGGGGCGCTATGACATCAATATGTGATGAGTGCCACTCAACTGACTCGACCACT	2700
QY	2701	ATCTGGGCACTCGGCAAGTCTGAGCAAGCGGAGAGCGGTGAGCGCGACTGCTGTCG	2760
Db	2701	ATCTGGGCACTCGGCAAGTCTGAGCAAGCGGAGAGCGGTGAGCGCGACTGCTGTCG	2760
QY	2761	CTGCCACCGCTAGCGCTCGGGATCGGTCACTGCGTCCACATCAACATCGAGAGGTG	2820
Db	2761	CTGCCACCGCTAGCGCTCGGGATCGGTCACTGCGTCCACATCAACATCGAGAGGTG	2820
QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCTCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCTCATCGAGACCATC	2880
QY	2881	AAGGGGGGAGGACCTCATTTCTGCAATTCGCAATTCGAAGAAATGTGATGAGCTCGCGCG	2940
Db	2881	AAGGGGGGAGGACCTCATTTCTGCAATTCGCAATTCGAAGAAATGTGATGAGCTCGCGCG	2940
QY	2941	AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCGGTC	3000
Db	2941	AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCGGTC	3000

QY	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACGGACGCTCTAATGACGGCTTTTACC	3060
Db	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACGGACGCTCTAATGACGGCTTTTACC	3060
QY	3061	GGCGATTTTCGACTCAGTGTGATCGACTGCAATCATGTGTCCACGACACTGCACTTCAGC	3120
Db	3061	GGCGATTTTCGACTCAGTGTGATCGACTGCAATCATGTGTCCACGACACTGCACTTCAGC	3120
QY	3121	CTGGACCGGACCTTCACTTGTGAGACGACGACCGGTGCCAAGACGCGGTGTACGCTCG	3180
Db	3121	CTGGACCGGACCTTCACTTGTGAGACGACGACCGGTGCCAAGACGCGGTGTACGCTCG	3180
QY	3181	CAGCGCGGAGGACGACTGTGTAGGGGAGGATGGGCAATTTACAGTTTGTGATCCAGGA	3240
Db	3181	CAGCGCGGAGGACGACTGTGTAGGGGAGGATGGGCAATTTACAGTTTGTGATCCAGGA	3240
QY	3241	GAACCGGCTTCCGGCATGTTTCGATTTCTCGGTTCGTGCGAGTGTATGACGCGGGCTGT	3300
Db	3241	GAACCGGCTTCCGGCATGTTTCGATTTCTCGGTTCGTGCGAGTGTATGACGCGGGCTGT	3300
QY	3301	GCTTGGTACGAGCTCACGCCCGCGGAGACCTCAGTTAGGTTCGCGGCTTACCTAAACACA	3360
Db	3301	GCTTGGTACGAGCTCACGCCCGCGGAGACCTCAGTTAGGTTCGCGGCTTACCTAAACACA	3360
QY	3361	CCAGGTTTCCCGCTCTGCGGACCACTCTGAGGACCATCTGGAGTTCTGGGAGGCTTTTACAGGCTTC	3420
Db	3361	CCAGGTTTCCCGCTCTGCGGACCACTCTGAGGACCATCTGGAGTTCTGGGAGGCTTTTACAGGCTTC	3420
QY	3421	ACCCACATAGACGCGCTTCTTGTGCCAGACTAAGCAGGCGAGGAGCACTTCCCTCCCTAC	3480
Db	3421	ACCCACATAGACGCGCTTCTTGTGCCAGACTAAGCAGGCGAGGAGCACTTCCCTCCCTAC	3480
QY	3481	CTGTTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGAC	3540
Db	3481	CTGTTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGAC	3540
QY	3541	CAAAATGGAAGTGTCTCATACGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCT	3600
Db	3541	CAAAATGGAAGTGTCTCATACGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCT	3600
QY	3601	TATAGGCTGGGAGCGCTTCAAAACGAGTTACTACCAACACACCCCTTAACCAATACATC	3660
Db	3601	TATAGGCTGGGAGCGCTTCAAAACGAGTTACTACCAACACACCCCTTAACCAATACATC	3660
QY	3661	ATGSCATGATGTCGCTGACCTGAGGTGCTACAGGACCTCGGTGCTGTTAGGCGGA	3720
Db	3661	ATGSCATGATGTCGCTGACCTGAGGTGCTACAGGACCTCGGTGCTGTTAGGCGGA	3720
QY	3721	GTCTTAGCAGCTTGGCGCGTATTGCTGACAAACAGGCGGTGCTATGTTGGGCGAGG	3780
Db	3721	GTCTTAGCAGCTTGGCGCGTATTGCTGACAAACAGGCGGTGCTATGTTGGGCGAGG	3780
QY	3781	ATCATCTTGTCCGAGGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Db	3781	ATCATCTTGTCCGAGGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
QY	3841	GATGAGATGGAAGTGGCGCTCACACCTCCCTTACATCGAACAGGGAATGCGCTCGCC	3900
Db	3841	GATGAGATGGAAGTGGCGCTCACACCTCCCTTACATCGAACAGGGAATGCGCTCGCC	3900
QY	3901	GAACAATTCACAGAGGCAATCGGTTGCTGCAACACGCGCCCAAGAGCGGAGGCT	3960
Db	3901	GAACAATTCACAGAGGCAATCGGTTGCTGCAACACGCGCCCAAGAGCGGAGGCT	3960
QY	3961	GCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGCGAGGATATG	4020
Db	3961	GCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGCGAGGATATG	4020
QY	4021	TGGAATTTTATCAGCGGATACAAATTTTATGAGGCTTGTCCACTCTGCTGCGCAACCCC	4080
Db	4021	TGGAATTTTATCAGCGGATACAAATTTTATGAGGCTTGTCCACTCTGCTGCGCAACCCC	4080
QY	4081	GGCATAGCATCACTGATGCAATTCACGCTTATCACCGCGCGCTCACCCCAACAT	4140

PT Cell culture system for hepatitis C virus, useful e.g. in screening for
 PT therapeutic agents, comprises human hepatoma cells containing a viral RNA
 PT construct that includes a selectable gene.

XX Claim 8; Page 37-43; 58pp; German.

XX This invention describes a novel Hepatitis C virus (HCV) cell culture
 CC system comprising human hepatoma cells that contain an integrated HCV-RNA
 CC construct (I). (I) contains the HCV-specific RNA segments 5'-NTR (non-
 CC translated region), NS (non-structural)3, NS4A, NS4B, NS5A, NS5B and 3'-
 CC NTR, and a selectable (marker) gene (II). The cell cultures, and/or (I),
 CC are used to prepare, evaluate and/or test therapeutic and/or diagnostic
 CC agents for HCV infections, and to prepare vaccines against HCV infection
 CC (particularly preparation of attenuated HCV). The can also be used for
 CC preparation of a liver-specific delivery system for gene therapy, and to
 CC identify cells permissive for HCV replication. Virus RNA replicates
 CC autonomously in and with high efficiency in this cellular system, so that
 CC variations in replication rates can be measured (for screening antiviral
 CC agents) quantitatively or qualitatively, using standard laboratory
 CC equipment. Efficient replication of HCV RNA is only achieved when the
 CC specified RNA segments are present and when the transfected cells are
 CC maintained under permanent selection pressure

XX Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7982.6; DB 3; Length 7989;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	GCAGCCCCCGATTGGGGGCGACACCTCCACCATAGATCACTCCCTGTGAGGAACCTACTG	60
DB	1	GCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG	60
QY	61	TCTTACGACGAAAGCGTCTAGCCATGGCGTTAGTATAGTGTGTCGAGCCCTCCAGGAC	120
DB	61	TCTTACGACGAAAGCGTCTAGCCATGGCGTTAGTATAGTGTGTCGAGCCCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGGCCATAGTGTCTGCGAAACCGGTGACTACACCGGAATGCCAG	180
DB	121	CCCCCTCCCGGAGGCCATAGTGTCTGCGAAACCGGTGACTACACCGGAATGCCAG	180
QY	181	GACGACCGGTCTCTTTCGATCAACCCCGCTCAATGCCCTGGAGATTGGGGGTGCCCCC	240
DB	181	GACGACCGGTCTCTTTCGATCAACCCCGCTCAATGCCCTGGAGATTGGGGGTGCCCCC	240
QY	241	GCAGACTGCTAGCCGAGTAGTGTGGTTCGAAAGGCCCTTGTGTAATCGCTGATAGG	300
DB	241	GCAGACTGCTAGCCGAGTAGTGTGGTTCGAAAGGCCCTTGTGTAATCGCTGATAGG	300
QY	301	GTGCTTCGAGTGCCTCCGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCCTAAC	360
DB	301	GTGCTTCGAGTGCCTCCGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCCTAAC	360
QY	361	CTCAAGAAAAAACAAGGGCGGCGCCATGATTGAAACAAGATGGATTGCACGAGGTCTC	420
DB	361	CTCAAGAAAAAACAAGGGCGGCGCCATGATTGAAACAAGATGGATTGCACGAGGTCTC	420
QY	421	CGGCGGCTTCGGTGGAGAGGCTATTTCGGCTATGATCTGGGCAACAAGACAAATCGGCTGCT	480
DB	421	CGGCGGCTTCGGTGGAGAGGCTATTTCGGCTATGATCTGGGCAACAAGACAAATCGGCTGCT	480
QY	481	CTGATGCGCGGTGTTCCGGCTGTCCGAGGGGCGCCCGGTCTCTTTTGTCAAGACCG	540
DB	481	CTGATGCGCGGTGTTCCGGCTGTCCGAGGGGCGCCCGGTCTCTTTTGTCAAGACCG	540
QY	541	ACCTGTCCGGTCCCTGAATGAATGAACTGACGAGGAGGCGGCTATCGTGGCTGGCCA	600
DB	541	ACCTGTCCGGTCCCTGAATGAATGAACTGACGAGGAGGCGGCTATCGTGGCTGGCCA	600
QY	601	CGAGGGGCTTCCTTGGCAGCTGTCTCGACGTTGTCACTGAGCGGAGGAGGACTGGC	660
DB	601	CGAGGGGCTTCCTTGGCAGCTGTCTCGACGTTGTCACTGAGCGGAGGAGGACTGGC	660

QY	661	TGCTATTGGCGAAGTGCCTGGGGGAGGATCTCCTGTGTATCTACCTTCTCTCTGCGGAGA	720
DB	661	TGCTATTGGCGAAGTGCCTGGGGGAGGATCTCCTGTGTATCTACCTTCTCTCTGCGGAGA	720
QY	721	AAGTATCCATCATGGCTGATCAATGCGGCGGCTGCATACGCTTGCATCGGCTACTGCTGC	780
DB	721	AAGTATCCATCATGGCTGATCAATGCGGCGGCTGCATACGCTTGCATCGGCTACTGCTGC	780
QY	781	CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC	840
DB	781	CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC	840
QY	841	TTTTCGATCAGGATGATCTGACGAGAGCATCAGGGGTCCGCGAGCGCACTGTTTCG	900
DB	841	TTTTCGATCAGGATGATCTGACGAGAGCATCAGGGGTCCGCGAGCGCACTGTTTCG	900
QY	901	CCAGCTCAAGCGCGCATGCGCGAGGAGTCTCGTGTGACCCATGCGATGCGTTC	960
DB	901	CCAGCTCAAGCGCGCATGCGCGAGGAGTCTCGTGTGACCCATGCGATGCGTTC	960
QY	961	GCTTCCCGAATATCATGTGTGAAATGCGCGCTTTTCTGGAATTCATCGACTGTGGCGGC	1020
DB	961	GCTTCCCGAATATCATGTGTGAAATGCGCGCTTTTCTGGAATTCATCGACTGTGGCGGC	1020
QY	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCGTGGCTACCGTGATATGCTGAAGAGC	1080
DB	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCGTGGCTACCGTGATATGCTGAAGAGC	1080
QY	1081	TTGGCGGCGAATGGGCTGACCGCTTCTGCTTACGGTATCGCGCTCCGATTCGC	1140
DB	1081	TTGGCGGCGAATGGGCTGACCGCTTCTGCTTACGGTATCGCGCTCCGATTCGC	1140
QY	1141	AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAG	1200
DB	1141	AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAG	1200
QY	1201	GTTTCCCTTAGCGGATCAATTCGCGCCCTTCCCTCCCGCCCCCTTAACGTTCTGCG	1260
DB	1201	GTTTCCCTTAGCGGATCAATTCGCGCCCTTCCCTCCCGCCCCCTTAACGTTCTGCG	1260
QY	1261	CGNAGCGCTTGGAAATAGCGCGGTGTGCTATATGTTATTTTCCACATATG	1320
DB	1261	CGNAGCGCTTGGAAATAGCGCGGTGTGCTATATGTTATTTTCCACATATG	1320
QY	1321	CCGTCTTTTGGCAATGTGAGGCGCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT	1380
DB	1321	CCGTCTTTTGGCAATGTGAGGCGCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT	1380
QY	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGGAAGGAGCA	1440
DB	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGGAAGGAGCA	1440
QY	1441	GTTTCCCTTGGAGCTTCTTGAAGACAAACAACTCTGTAGCGACCTTTTCAGCGAGCGG	1500
DB	1441	GTTTCCCTTGGAGCTTCTTGAAGACAAACAACTCTGTAGCGACCTTTTCAGCGAGCGG	1500
QY	1501	AACCCCGCACTCGCGACAGGTCCCTCTGCGGCAAAAGCCACCTGTATAGATACACCT	1560
DB	1501	AACCCCGCACTCGCGACAGGTCCCTCTGCGGCAAAAGCCACCTGTATAGATACACCT	1560
QY	1561	GCAAGCGGCGCAACACCCGAGTGTGAGTGTGATGTGGAAGAGTCAAA	1620
DB	1561	GCAAGCGGCGCAACACCCGAGTGTGAGTGTGATGTGGAAGAGTCAAA	1620
QY	1621	TGGCTCTCCCTCAAGCGTATTCAACAGGGGCTCAAGGATCCCAAGAGGTACCCCAATTGT	1680
DB	1621	TGGCTCTCCCTCAAGCGTATTCAACAGGGGCTCAAGGATCCCAAGAGGTACCCCAATTGT	1680
QY	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTTGTAGTGTGAGTTTAAA	1740
DB	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTTGTAGTGTGAGTTTAAA	1740
QY	1741	AACGTCTAGGCCCCCCCCGAAACCGAGGAGCGTGGTTTTTCTTTGAAAAAACACGATAATACC	1800

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1801 ATGGGCGCTATTACGGCTTACTCCACAGACGAGGCTACTTGGCTGCAATCACT 1860
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1861 AGCCTCACAGGCGGACAGAAACAGGTCGAGGGGAGGTCCAGGTGTCCTCCACCGCA 1920
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1921 ACACAATCTTCTGGCGACCTCGCTCAATGCGGTGTGTGGACTGTCTATCATGCTGCC 1980
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3421 ACCCACAATAGACGCGCTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
3421 ACCCACAATAGACGCGCTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
3481 CTGCTAGCATACAGGCTACCGGTGTCGCGCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
3481 CTGCTAGCATACAGGCTACCGGTGTCGCGCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
3541 CAAATGTGGAGTCTCTCATACGCTAAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 3600
3541 CAAATGTGGAGTCTCTCATACGCTAAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 3600
3601 TATAGGCTGGAGCGCTTCAAAACGAGTTTACTACCAACACCCCAATAACCAATACATC 3660
3601 TATAGGCTGGAGCGCTTCAAAACGAGTTTACTACCAACACCCCAATAACCAATACATC 3660
3661 ATGSCATGCTGCGGTGACCTGAGAGTGTGTCAGAGACCTGGGTGCTGGTAGGCGGA 3720
3661 ATGSCATGCTGCGGTGACCTGAGAGTGTGTCAGAGACCTGGGTGCTGGTAGGCGGA 3720
3721 GTCCTAGCAGCTGCGCGCGTATTGCTGACAAACGAGCGGTGCTATTGTGGGCGG 3780
3721 GTCCTAGCAGCTGCGCGCGTATTGCTGACAAACGAGCGGTGCTATTGTGGGCGG 3780
3781 ATCATCTGTCGGAAGCGGCTCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC 3840
3781 ATCATCTGTCGGAAGCGGCTCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC 3840
3841 GATGAGTGAAGTGGCTCAGCTCCCTTATCATCGAAACAGGGAATGCACTCGCC 3900
3841 GATGAGTGAAGTGGCTCAGCTCCCTTATCATCGAAACAGGGAATGCACTCGCC 3900
3901 GAAACAATCAACAGAGGCAATCGGTTCTGCAACAGCCCAAGCAAGCGGAGGCT 3960
3901 GAAACAATCAACAGAGGCAATCGGTTCTGCAACAGCCCAAGCAAGCGGAGGCT 3960

Db	6121		CTGGCGCAGAAGAAGGTCACCTTTTGACAGACTGCAGGTCTCTGGACGACCACTACCGG	6180
Qy	6181		GTGCTCTAAGGAGATGAAGGCGAAGCGCTCCACAGCTTAAGGCTAACTTCTATCCGTGGAG	6240
Db	6181		GTGCTCAAGGAGATGAAGGCGAAGCGCTCCACAGCTTAAGGCTAACTTCTATCCGTGGAG	6240
Qy	6241		GAAGCTCTTAAGCTGACGCCGCCCACTTCGGCCAGATCTAAATTTGGCTATGGGCGAAAG	6300
Db	6241		GAAGCTCTTAAGCTGACGCCGCCCACTTCGGCCAGATCTAAATTTGGCTATGGGCGAAAG	6300
Qy	6301		GACCTCCGGAACCTTATCCAGCAAGGCGGTAAACCAATCCGCTCCGTGTGGAGGACTTG	6360
Db	6301		GACCTCCGGAACCTTATCCAGCAAGGCGGTAAACCAATCCGCTCCGTGTGGAGGACTTG	6360
Qy	6361		CTGGAAGACACTGAGACACCAATTTGACACCAACCATATGSCAAAAATAGGTTTCTGC	6420
Db	6361		CTGGAAGACACTGAGACACCAATTTGACACCAACCATATGSCAAAAATAGGTTTCTGC	6420
Qy	6421		GTCCAACGAGAAAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTCCAGATTTGGGG	6480
Db	6421		GTCCAACGAGAAAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTCCAGATTTGGGG	6480
Qy	6481		GTTCGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCCGTG	6540
Db	6481		GTTCGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCCGTG	6540
Qy	6541		ATGGGCTCTTCAATACCGATTCCAATATCTCTCTGGACAGCGGTTCGAGTTCTCTGGTGAAT	6600
Db	6541		ATGGGCTCTTCAATACCGATTCCAATATCTCTCTGGACAGCGGTTCGAGTTCTCTGGTGAAT	6600
Qy	6601		GCTTGGAAAGCGAAGAAATGCCCTTATGGGCTTCGATATGACACCCGCTGTTTGA	6660
Db	6601		GCTTGGAAAGCGAAGAAATGCCCTTATGGGCTTCGATATGACACCCGCTGTTTGA	6660
Qy	6661		ACGCTCACTGAGATGACATCCGTGTGAGAGTCAATCTACCAATGTGTGACTTGGCC	6720
Db	6661		ACGCTCACTGAGATGACATCCGTGTGAGAGTCAATCTACCAATGTGTGACTTGGCC	6720
Qy	6721		CCCGAAGCCAGACAGGCGTAAAGTGCTCTCACAGAGCGGTTTACATCGGGCGCCCTG	6780
Db	6721		CCCGAAGCCAGACAGGCGTAAAGTGCTCTCACAGAGCGGTTTACATCGGGCGCCCTG	6780
Qy	6781		ACTAATTTAAAGGCGAAGACTCGGCTATCGCGGTCGCGCGAGCGGTGTACTGACG	6840
Db	6781		ACTAATTTAAAGGCGAAGACTCGGCTATCGCGGTCGCGCGAGCGGTGTACTGACG	6840
Qy	6841		ACGAGCTCGGTTAATACCTTCAATGTTTGAAGCGCGCTCGCGGCTGTGAGCTGG	6900
Db	6841		ACGAGCTCGGTTAATACCTTCAATGTTTGAAGCGCGCTCGCGGCTGTGAGCTGG	6900
Qy	6901		AAGCTCCAGACTGACGATGCTGTATGCGGAGACGACTTGTCTGTATCTGTGAAGC	6960
Db	6901		AAGCTCCAGACTGACGATGCTGTATGCGGAGACGACTTGTCTGTATCTGTGAAGC	6960
Qy	6961		GCGGGACCCAGAGACGAGGCGAGCCTACGGGCTTACGAGGCTATGACTAGATAC	7020
Db	6961		GCGGGACCCAGAGAGACGAGGCGAGCCTACGGGCTTACGAGGCTATGACTAGATAC	7020
Qy	7021		TCTGCCCCCTCGGGNACCGCCCAACCAAGATACGACTTGGAGTTGATATCATGTC	7080
Db	7021		TCTGCCCCCTCGGGNACCGCCCAACCAAGATACGACTTGGAGTTGATATCATGTC	7080
Qy	7081		TCCTCCAATGTGTCAGTCCGCGCAGATGATCTGGCAAAAGGTTGACTATCTCCCGT	7140
Db	7081		TCCTCCAATGTGTCAGTCCGCGCAGATGATCTGGCAAAAGGTTGACTATCTCCCGT	7140
Qy	7141		GACCCCAACACCCCTTGGCGGGCTGGTGGGACAGCTAGACACACTCCAGTCAAT	7200
Db	7141		GACCCCAACACCCCTTGGCGGGCTGGTGGGACAGCTAGACACACTCCAGTCAAT	7200
Qy	7201		TCCTGGCTAGGCAACATCATATGATATGCCCACTTGTGGCAAGGATGATCTCTGATG	7260

Db	7201	TCCTGGCTAGGCAACATCATGTATGCGCCACCTTGTGGGCAAGGATGATCCTGATG	7260
Qy	7261	ACTCATTTCTCTCCATCCTTCTAGCTCAGAAACAATTGAAAAGCCCTAGATTGTTCAG	7320
Db	7261		
Db	7261	ACTCATTTCTTCTCATCCTTCTAGCTCAGGAAACAATTGAAAAGCCCTAGATTGTTCAG	7320
Qy	7321	ATCTACGGGGCGCTGTTACTTCCATTTGAGCCACTTGCACCTTACTCTCAGATCANTTCACGACTC	7380
Db	7321	ATCTACGGGGCGCTGTTACTTCCATTTGAGCCACTTGCACCTTACTCTCAGATCANTTCACGACTC	7380
Qy	7381	CATGGCCTTAGCGCATTTTCTACCTCATAGTTACTCTCCAGTGAGATCAATTAGGGTGGCT	7440
Db	7381	CATGGCCTTAGCGCATTTTCTACCTCATAGTTACTCTCCAGTGAGATCAATTAGGGTGGCT	7440
Qy	7441	TCATGCCTCAGAAACTTTGGGGTACCGGCTTGGAGTCTGGAGACATTCGGGCCAGAAGT	7500
Db	7441	TCATGCCTCAGAAACTTTGGGGTACCGGCTTGGAGTCTGGAGACATTCGGGCCAGAAGT	7500
Qy	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGCAAGTACCTCTTC	7560
Db	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGCAAGTACCTCTTC	7560
Qy	7561	AATGGGGCAGTAAGACCAAGCTCAACTCCAATCCCGCTGGCTGCCAGTTGGAT	7620
Db	7561	AATGGGGCAGTAAGACCAAGCTCAACTCCAATCCCGCTGGCTGCCAGTTGGAT	7620
Qy	7621	TTATCCAGCTGGTTGGTTGCTGCTTACAGCGGGGAGACATATATCAACGCTGTCTCGT	7680
Db	7621	TTATCCAGCTGGTTGGTTGCTGCTTACAGCGGGGAGACATATATCAACGCTGTCTCGT	7680
Qy	7681	GCCCGACCCCGCTGGTTTCATGTGGTGGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCCGACCCCGCTGGTTTCATGTGGTGGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT	7740
Qy	7741	CTACTCCCAACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCCATCTCTGTTTT	7800
Db	7741	CTACTCCCAACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCCATCTCTGTTTT	7800
Qy	7801	TTTCCCTTTTTTTTTCTTTCTCTTTT	7860
Db	7801	TTTCCCTTTTTTTTTCTTTCTCTTTT	7860
Qy	7861	TTTTTCTCTTTTTTTTCTTTTTCTTTTCTTTTGGTGGCTCCATCTTAGCCCTAGTCAAGCC	7920
Db	7861	TTTTTCTCTTTTTTTTCTTTTTCTTTTCTTTTGGTGGCTCCATCTTAGCCCTAGTCAAGCC	7920
Qy	7921	TAGCTGTGAAGGTCCGTGAGCCGCTTGACTCAGAGAGTGTGTGATCTAGCCCTCTCTCG	7980
Db	7921	TAGCTGTGAAGGTCCGTGAGCCGCTTGACTCAGAGAGTGTGTGATCTAGCCCTCTCTCG	7980
Qy	7981	AGATCAAGT 7989	
Db	7981	AGATCAAGT 7989	
RESULT 11			
ABK91440			
ID	ABK91440 standard; DNA; 10690 BP.		
XX	AC ABK91440;		
XX	15-NOV-2002 (first entry)		
DT	Hepatitis C virus vector construct pHCVNeo.17m7.		
DE	HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;		
XX	hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;		
KW	internal ribosome entry site; IRES; NS5A; HCV replication; mutant.		
KW	Hepatitis C virus.		
OS	Encephalomyocarditis virus.		
OS	Escherichia coli.		
OS	Enterobacteria phage T7		

QY	3241	GAACGGCCCTCGGGCATGTTGGATTCCTGGTTCTGTGGAGTGTCTATGACGGGGCTGT	3300	Db	4321	TTTAAAGGTCAATGAGCGGGAGATGCCCTCCACCGAGGACCTGGTTAAACCTACTCCCTGCT	4380
Db	3241	GAACGGCCCTCGGGCATGTTGGATTCCTGGTTCTGTGGAGTGTCTATGACGGGGCTGT	3300	QY	4381	ATCCCTCTCCCTGGCGCCCTAGTCTCGGGGTCTGTGGAGGATCTGCTGGGAC	4440
QY	3301	GCTTGTGTACAGCTCACGCCGCCCGGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA	3360	Db	4381	ATCCCTCTCCCTGGCGCCCTAGTCTCGGGGTCTGTGGAGGATCTGCTGGGAC	4440
Db	3301	GCTTGTGTACAGCTCACGCCGCCCGGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA	3360	QY	4441	GTGGGCCAGAGGGAGGGGGCTGTGAGTGAATAAAGGGCTGATAGCGTTCTGCTTCGGGG	4500
QY	3361	CCAGGGTTCCCGTCTGCGAGAGCAATCTGGAGTCTGGAGAGCGTCTTTACAGGCCTC	3420	Db	4441	GTGGGCCAGAGGGAGGGGGCTGTGAGTGAATAAAGGGCTGATAGCGTTCTGCTTCGGGG	4500
Db	3361	CCAGGGTTCCCGTCTGCGAGAGCAATCTGGAGTCTGGAGAGCGTCTTTACAGGCCTC	3420	QY	4501	GCTTAACACAGCTCTCCCGCACCTATGTGCTTGAGAGGAGCGCTGACGATGTGCTT	4560
QY	3421	ACCCATAGAGCCCAATCTTGTGCCAGATTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Db	4501	GCTTAACACAGCTCTCCCGCACCTATGTGCTTGAGAGGAGCGCTGACGATGTGCTT	4560
Db	3421	ACCCATAGAGCCCAATCTTGTGCCAGATTAAGCAGCAGGAGACAACTTCCCTTAC	3480	QY	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC	4620
QY	3481	CTGGTAGCATACAGGCTACGGTGTGGCGCAGGGCTCAGGCTCCACTCCATCGTGGGAC	3540	Db	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC	4620
Db	3481	CTGGTAGCATACAGGCTACGGTGTGGCGCAGGGCTCAGGCTCCACTCCATCGTGGGAC	3540	QY	4621	GAGGACTGTCTCCACGCAATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGC	4680
QY	3541	CAAAATGTGAAGTGTCTATACGGCTAAAGCTTACCTGCAACAGCCCAACCAATACATC	3600	Db	4621	GAGGACTGTCTCCACGCAATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGC	4680
Db	3541	CAAAATGTGAAGTGTCTATACGGCTAAAGCTTACCTGCAACAGCCCAACCAATACATC	3600	QY	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCCAGTCCGCGGATTTGCCGGGA	4740
QY	3601	TATAGCTGGAGCGCTTCAAAACAGAGTTTACCCACACACACCCCAACCAATACATC	3660	Db	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCCAGTCCGCGGATTTGCCGGGA	4740
Db	3601	TATAGCTGGAGCGCTTCAAAACAGAGTTTACCCACACACACCCCAACCAATACATC	3660	QY	4741	GTCCCTCTTCTCATGTCAAGCTGAGGAGTCTGGCGGGGCGACGCAATCATG	4800
QY	3661	ATGGCATGATGTGGCTGACCTGAGGTGCTCACGAGCACCTGGGTGCTGGTAGCGGA	3720	Db	4741	GTCCCTCTTCTCATGTCAAGCTGAGGAGTCTGGCGGGGCGACGCAATCATG	4800
Db	3661	ATGGCATGATGTGGCTGACCTGAGGTGCTCACGAGCACCTGGGTGCTGGTAGCGGA	3720	QY	4801	CAAAACACCTGCGCATGTGGAGCACAGATCACCGGACATGTGAAACCGGTTCCATGAGG	4860
QY	3721	GTCTTAGAGCTGTGGCGGGTATTCCTGACAAAGGAGGCTGCTTACCGGGAGTTC	3780	Db	4801	CAAAACACCTGCGCATGTGGAGCACAGATCACCGGACATGTGAAACCGGTTCCATGAGG	4860
Db	3721	GTCTTAGAGCTGTGGCGGGTATTCCTGACAAAGGAGGCTGCTTACCGGGAGTTC	3780	QY	4861	ATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCGCCATTAACGGGTAC	4920
QY	3781	ATCATCTGTTCGGAAGCGGGCCATCATTCGCGACAGGGAAGTCTTTACCGGGAGTTC	3840	Db	4861	ATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCGCCATTAACGGGTAC	4920
Db	3781	ATCATCTGTTCGGAAGCGGGCCATCATTCGCGACAGGGAAGTCTTTACCGGGAGTTC	3840	QY	4921	ACCAAGCGGCTTCCAGCGGCTCCCGGCGCCAAATTTCTAGGGCGCTGTGGCGGGTG	4980
QY	3841	GATGAGATGAAGAGTGCCTCACACCTCCCTTACATCGAAACAGGGAATGCAAGTCCGC	3900	Db	4921	ACCAAGCGGCTTCCAGCGGCTCCCGGCGCCAAATTTCTAGGGCGCTGTGGCGGGTG	4980
Db	3841	GATGAGATGAAGAGTGCCTCACACCTCCCTTACATCGAAACAGGGAATGCAAGTCCGC	3900	QY	4981	GCTGTGAGAGTACCTGAGGTTTACCGGGTGGGGATTTCCACTACGTACGAGGATG	5040
QY	3901	GAACAAATCAACAGAGGAATCGGGTGTCTGCAACAGCCACCAAGCAGGAGGCT	3960	Db	4981	GCTGTGAGAGTACCTGAGGTTTACCGGGTGGGGATTTCCACTACGTACGAGGATG	5040
Db	3901	GAACAAATCAACAGAGGAATCGGGTGTCTGCAACAGCCACCAAGCAGGAGGCT	3960	QY	5041	ACCACTGAACAAAGTAAAGTCCCGGTTCGGGCGCCCGGAAATTTCTTCAAGAGTG	5100
QY	3961	GCTGCTCCGCTGGAATCCAAAGTGGGAGCCTCGAAGCCTTCTGGGCGAAGCATATG	4020	Db	5041	ACCACTGAACAAAGTAAAGTCCCGGTTCGGGCGCCCGGAAATTTCTTCAAGAGTG	5100
Db	3961	GCTGCTCCGCTGGAATCCAAAGTGGGAGCCTCGAAGCCTTCTGGGCGAAGCATATG	4020	QY	5101	GATGGGTGGGTTCGACAGGTACGCTCCAGCGTGAACCCCTCTTACGGGAGGAGTTC	5160
QY	4021	TGGAATTTATCAGCGGGATACAAATTTTAGAGGCTTGTCCACTCTGCTGCGAAGCCCC	4080	Db	5101	GATGGGTGGGTTCGACAGGTACGCTCCAGCGTGAACCCCTCTTACGGGAGGAGTTC	5160
Db	4021	TGGAATTTATCAGCGGGATACAAATTTTAGAGGCTTGTCCACTCTGCTGCGAAGCCCC	4080	QY	5161	ACATTTCTGCTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCATCGAGGCGGAA	5220
QY	4081	GCATAGCATCTAGTGAATTCAGGCTTCTACAGCGCGCTTACCAACCCACAT	4140	Db	5161	ACATTTCTGCTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCATCGAGGCGGAA	5220
Db	4081	GCATAGCATCTAGTGAATTCAGGCTTCTACAGCGCGCTTACCAACCCACAT	4140	QY	5221	CCGGAAGTGGGTTCGACAGGTACGCTCCAGCGGCGGCGGCGGCGGAGAGG	5280
QY	4141	ACCTCTCTGTTTAAACATCTCTGGGGATGGGTGGCGCGCCCAACTTGTCTCCAGCGCT	4200	Db	5221	CCGGAAGTGGGTTCGACAGGTACGCTCCAGCGGCGGCGGCGGCGGAGAGG	5280
Db	4141	ACCTCTCTGTTTAAACATCTCTGGGGATGGGTGGCGCGCCCAACTTGTCTCCAGCGCT	4200	QY	5281	GCTTAAGCGTGGGTTCGAGGAGTCTCCCGGCTTCTTGGCGGAGCTCATCAGCTAGCCAG	5340
QY	4201	GCTTCTGCTTCTGAGCGCGGATTCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTTAAGCGTGGGTTCGAGGAGTCTCCCGGCTTCTTGGCGGAGCTCATCAGCTAGCCAG	5340
Db	4201	GCTTCTGCTTCTGAGCGCGGATTCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	QY	5341	CTGTCTGCGCTTCTTTGAAGGCAACATGCACTACCGGTCTGCTTCCCGGAGCGTGCAC	5400
QY	4261	AAGGTCTTCTGAGATTTTGGAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGCC	4320	Db	5341	CTGTCTGCGCTTCTTTGAAGGCAACATGCACTACCGGTCTGCTTCCCGGAGCGTGCAC	5400
Db	4261	AAGGTCTTCTGAGATTTTGGAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGCC	4320	QY	5401	CTCATCGAGGCGGAGTCTGTCGCGAGGAGTGGCGGGAACATCAACCGGCTGGAG	5460
QY	4321	TTTAAAGTTCATAGCGGGAGATGCCCTCCACCGAGGACCTGGCTAAACCTACTCCCTGCT	4380				

QY 7621 TTATCCAGCTGTTGCTGTTGCTGTTTACAGCGGGGAGACATATATCAGACCTGCTCTGCT 7680
 DB |||||||
 QY 7621 TTATCCAGCTGTTGCTGTTGCTGTTTACAGCGGGGAGACATATATCAGACCTGCTCTGCT 7680
 DB |||||||
 QY 7681 GCCCGACCCCGCTGCTTCAATGCTGCTGCTTACTCTTCTGCTAGGGGTAGGCATCTAT 7740
 DB |||||||
 QY 7681 GCCCGACCCCGCTGCTTCAATGCTGCTGCTTACTCTTCTGCTAGGGGTAGGCATCTAT 7740
 DB |||||||
 QY 7741 CTACTCCCAACCGATGAAACCGGGAGCTAAACACTCCAGGCCCAATAGGCCATCTGTTT 7800
 DB |||||||
 QY 7741 CTACTCCCAACCGATGAAACCGGGAGCTAAACACTCCAGGCCCAATAGGCCATCTGTTT 7800
 DB |||||||
 QY 7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 DB |||||||
 QY 7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 DB |||||||
 QY 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
 DB |||||||
 QY 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
 DB |||||||
 QY 7921 TAGCTGTGAAGGTCGCTGAGCGCTTGACTGTCAGAGAGTGTGATGCTGCTCTCTG 7980
 DB |||||||
 QY 7921 TAGCTGTGAAGGTCGCTGAGCGCTTGACTGTCAGAGAGTGTGATGCTGCTCTCTG 7980
 DB |||||||
 QY 7981 AGATCAAGTACT 7992
 DB |||||||
 QY 7981 AGATCAAGTACT 7992
 DB |||||||

RESULT 12

AAD25322

ID AAD25322 standard; cDNA; 7989 BP.

XX AC

AAD25322;

12-MAR-2002 (first entry)

Hepatitis C virus (HCV) replBartMan/AvaII cDNA.

XX Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 KW gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 KW ss.

Hepatitis C virus.

XX Key Location/Qualifiers

FH CDS 1801..7758

FT /*tag= a

FT /product= "HCVreplBartMan polyprotein"

FT 7766

FT /*tag= b

FT /note= "Nucleotide creating AvaII site"

XX WD200189364-A2.

XX PD

XX PD

XX PD

PF 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US016822.

XX 23-MAY-2000; 2000US-00576989.

XX (UNIW) UNIV WASHINGTON.

XX PI Rice CM, Blight KJ;

XX DR WPI; 2002-066755/09.

XX DR P-PSDB; AAE15717.

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The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polyprotein coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for the generation of defined HCV virus stocks to develop in vitro and in vivo assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficiency replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated HCV derivatives as possible vaccine candidates, engineering of attenuated or defective HCV derivatives for expression of heterologous gene products for gene therapy and vaccine applications and for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) replBartMan/AvaII cDNA

XX SQ Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 U; 0 Other;

Query Match

Best Local Similarity 99.9%; Score 7981; DB 6; Length 7989;

Matches 7984; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
 DB |||||||
 QY 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
 DB |||||||
 QY 61 TCTTACCGCAGAAAGCGTCTAGCCATGGCTTGTAGTATGAGTGTGTCGTCAGCCCTCCAGGAC 120
 DB |||||||
 QY 61 TCTTACCGCAGAAAGCGTCTAGCCATGGCTTGTAGTATGAGTGTGTCGTCAGCCCTCCAGGAC 120
 DB |||||||
 QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAAACCGGTGAGTACACCGGAATGCCAG 180
 DB |||||||
 QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAAACCGGTGAGTACACCGGAATGCCAG 180
 DB |||||||
 QY 181 GACGACCGGGTCTTTCTTGGATCAACCGGCTCAATGCTTGGAGATTTGGGGTGGCCCC 240
 DB |||||||
 QY 181 GACGACCGGGTCTTTCTTGGATCAACCGGCTCAATGCTTGGAGATTTGGGGTGGCCCC 240
 DB |||||||
 QY 241 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAAGGCTTGTGCTACTGCTGATAGG 300
 DB |||||||
 QY 241 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAAGGCTTGTGCTACTGCTGATAGG 300
 DB |||||||
 QY 301 GTGCTTTGCGAGTGCCCCCGGAGGTCTCGTAGACCGTGCACCATAGAGCAAAATCTAAAC 360
 DB |||||||
 QY 301 GTGCTTTGCGAGTGCCCCCGGAGGTCTCGTAGACCGTGCACCATAGAGCAAAATCTAAAC 360
 DB |||||||
 QY 361 CTCAAAGAAAACCAAGGGCGGCCATGATTTGAACAAGATGATTTGTCAGCGAGTTCTC 420
 DB |||||||
 QY 361 CTCAAAGAAAACCAAGGGCGGCCATGATTTGAACAAGATGATTTGTCAGCGAGTTCTC 420
 DB |||||||
 QY 421 CGGCCGCTTGGGTGGAGAGGCTATTCCGCTTATGACTGGGGCACAACAGAAATCGGCTGCT 480
 DB |||||||
 QY 421 CGGCCGCTTGGGTGGAGAGGCTATTCCGCTTATGACTGGGGCACAACAGAAATCGGCTGCT 480
 DB |||||||
 QY 481 CTGATCCGCGGTGTTTCCGCTGTGACGCGAGGGCGCCGGTCTCTTTTGTCAAGACCG 540
 DB |||||||
 QY 481 CTGATCCGCGGTGTTTCCGCTGTGACGCGAGGGCGCCGGTCTCTTTTGTCAAGACCG 540
 DB |||||||
 QY 541 ACCTGTCCGGTGGCCCTGMACTGAACTCAGGACGAGCGCGCTATCTGTGCTGGCCA 600
 DB |||||||

Hepatitis C virus variants having greater transfection efficiency and ability to survive subpassage, useful as a vaccine for immunizing primate to the virus, comprise non-naturally occurring viral sequences.

Claim 44; Page 69-71; 174pp; English.

541	ACCTGTCCGTCCTGAATGAACATGACAGACGAGCGAGCGCGCTATCTGTGGCTGGCCA	600
QY	CGACGGCGTTCTTTGCGCAGCTGTGCTCGACGTTGTTCACATGAAGCGGGAAGGACTGGC	660
Db	CGACGGCGTTCTTTGCGCAGCTGTGCTCGACGTTGTTCACATGAAGCGGGAAGGACTGGC	660
QY	TGCTATTGGGCGAAGTGGCGGGGAGAGATCTCTGTCTCATCTCACTCTCTCTCCGCGAGA	720
Db	TGCTATTGGGCGAAGTGGCGGGGAGGATCTCTGTCTCATCTCACCTTGCTCTCTCCGCGAGA	720
QY	AAGTATCCATCATGCTCATGCAATCGGCGGCTGCATACGTTGATTCGGCTACTGCTGCC	780
Db	AAGTATCCATCATGCTCATGCAATCGGCGGCTGCATACGTTGATTCGGCTACTGCTGCC	780
QY	CATTTCAGACCAACAAACGAAAAATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTC	840
Db	CATTTCAGACCAACAAACGAAAAATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTC	840
QY	TTGTTCGATCAGGATGATCTGGAACGAAGAGCATCAGGGGCTCGGCCACGCGAACTGTTGC	900
Db	TTGTTCGATCAGGATGATCTGGAACGAAGAGCATCAGGGGCTCGGCCACGCGAACTGTTGC	900
QY	CCAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGGTCAACCATGGCGCATGCTCT	960
Db	CCAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGGTCAACCATGGCGCATGCTCT	960
QY	GCTTCCGAATATCATGTTGAAAAATGGCCGCTTTCTGGATTTCATCGACTGTGGCCGCGC	1020
Db	GCTTCCGAATATCATGTTGAAAAATGGCCGCTTTCTGGATTTCATCGACTGTGGCCGCGC	1020
QY	TGGTGTGGCGGACGGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC	1080
Db	TGGTGTGGCGGACGGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC	1080
QY	TTGGCGGCGAATGGGCTCACCGCTTCCTCGTCTTACGTTACGCTATCGCCGCTCCCGATTTCG	1140
Db	TTGGCGGCGAATGGGCTCACCGCTTCCTCGTCTTACGTTACGCTATCGCCGCTCCCGATTTCG	1140
QY	AGCGCATCGCCTTCTATCGCCTTCTTGACAGAGTTCTTCTGAGTTTAAACAGACCACAAGC	1200
Db	AGCGCATCGCCTTCTATCGCCTTCTTGACAGAGTTCTTCTGAGTTTAAACAGACCACAAGC	1200
QY	GTTTCCCTCTAGCGGGATCAATTCCGCGCCTCTCCCTCCCCCCCCCTAACTGTTACTGGC	1260
Db	GTTTCCCTCTAGCGGGATCAATTCCGCGCCTCTCCCTCCCCCCCCCTAACTGTTACTGGC	1260
QY	CGAAGCGCTTGGATAAGCGCGGTGCGTTGTCTATATGTTATTTTCCACGATATTG	1320
Db	CGAAGCGCTTGGATAAGCGCGGTGCGTTGTCTATATGTTATTTTCCACGATATTG	1320
QY	CCGTCCTTTTGCGCAATGTGAGGGGCCGGAACCTGGCGCTCTCTTCTTGACGAGCATTCCT	1380
Db	CCGTCCTTTTGCGCAATGTGAGGGGCCGGAACCTGGCGCTCTCTTCTTGACGAGCATTCCT	1380
QY	AGGGGCTTTTCCCTCTCGCCCAAGGAATGCAAGTCTGTTGAATGTCGTGAAGGAGCA	1440
Db	AGGGGCTTTTCCCTCTCGCCCAAGGAATGCAAGTCTGTTGAATGTCGTGAAGGAGCA	1440
QY	GTTCTCTGGAAGCTTCTTGACACAACACGTTCTGACGACCTTTTCAGCGACGCG	1500
Db	GTTCTCTGGAAGCTTCTTGACACAACACGTTCTGACGACCTTTTCAGCGACGCG	1500
QY	AACCCCCACCTGGCGACAGTGGCTCTGGGGCCAAAGCCACGTTATTAAGATACACCT	1560
Db	AACCCCCACCTGGCGACAGTGGCTCTGGGGCCAAAGCCACGTTATTAAGATACACCT	1560
QY	GCAAGGGCGGCAACCCCCAGTGCAGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA	1620
Db	GCAAGGGCGGCAACCCCCAGTGCAGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA	1620
QY	TGGCTCTCCTCAAGCGTATTCAACAAAGGGGCTGAAGTGCAGAGGTAAGTACCCCATTTGT	1680
Db	TGGCTCTCCTCAAGCGTATTCAACAAAGGGGCTGAAGTGCAGAGGTAAGTACCCCATTTGT	1680

4921	DB	ACCACGGGCCCTGCAAGCCCTCCCGCGCGCCAAATTATTCTAGGGCGCTGTGGCGGGT	498
4981	QY	GCTGCTGAGGAGTAGCTGGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGCATG	5040
4981	DB	GCTGCTGAGGAGTAGCTGGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGCATG	5040
5041	QY	ACCACTGACAACGTAAAGTGGCCGTGTACAGTTCCGGGCCCCGAAATTTCTTCAAGAAGTG	5100
5041	DB	ACCACTGACAACGTAAAGTGGCCGTGTACAGTTCCGGGCCCCGAAATTTCTTCAAGAAGTG	5100
5101	QY	GATGGGGTCCGGTTGCGACAGAGTAGCGTCCACGCGTGCAGAACCCCTCTACCGGAGGAGTTC	5160
5101	DB	GATGGGGTCCGGTTGCGACAGAGTAGCGTCCACGCGTGCAGAACCCCTCTACCGGAGGAGTTC	5160
5161	QY	ACATTCCTGGTCCGGCTCAATCAATCACTGTGTTGGGTACAGAGTCCCATCGGAGCCCGAA	5220
5161	DB	ACATTCCTGGTCCGGCTCAATCAATCACTGTGTTGGGTACAGAGTCCCATCGGAGCCCGAA	5220
5221	QY	CGGACGTAGCAGTGTCTCACTTCATGTCTACCGACCCCTCCCACTTACGGCGGAGACG	5280
5221	DB	CGGACGTAGCAGTGTCTCACTTCATGTCTACCGACCCCTCCCACTTACGGCGGAGACG	5280
5281	QY	GCTAAGCGTAGCGTGGCCAGGGGATCTCCCCCTCTTGGCGAGCTCATCAGTGTGCCAG	5340
5281	DB	GCTAAGCGTAGCGTGGCCAGGGGATCTCCCCCTCTTGGCGAGCTCATCAGTGTGCCAG	5340
5341	QY	CTGTCTGGCCCTTCCTTTGAAGGCAACATGCACTACCCGTCTGACATCCCCGGACGCTGAC	5400
5341	DB	CTGTCTGGCCCTTCCTTTGAAGGCAACATGCACTACCCGTCTGACATCCCCGGACGCTGAC	5400
5401	QY	CTCATCAGAGGCAACCTCTGTGTGGCGCAGAGATGGGCGGGAACTCATCCCGCTGGAG	5460
5401	DB	CTCATCAGAGGCAACCTCTGTGTGGCGCAGAGATGGGCGGGAACTCATCCCGCTGGAG	5460
5461	QY	TCGAAAATAAGGTAGTAAATTTTGGACTCTTTTGAGCGCTCCAAAGGGGAGGATGAG	5520
5461	DB	TCGAAAATAAGGTAGTAAATTTTGGACTCTTTTGAGCGCTCCAAAGGGGAGGATGAG	5520
5521	QY	AGGGAAGTATCCGTTCCGGCGGAGATCTCTCGGAGGTTCCAGGAAATTTCCCTCGAGCGATG	5580
5521	DB	AGGGAAGTATCCGTTCCGGCGGAGATCTCTCGGAGGTTCCAGGAAATTTCCCTCGAGCGATG	5580
5581	QY	CCCATATGGGACGCGCCGGATTAACAACCTTCCACTGTTAGAGTCTTGGAAGGACCCGGAC	5640
5581	DB	CCCATATGGGACGCGCCGGATTAACAACCTTCCACTGTTAGAGTCTTGGAAGGACCCGGAC	5640
5641	QY	TAGTCTCCTCCAGTGTGTACAGGGTGTCCATTGCGGCTTCCAAAGGCCCTTCGATACCA	5700
5641	DB	TAGTCTCCTCCAGTGTGTACAGGGTGTCCATTGCGGCTTCCAAAGGCCCTTCGATACCA	5700
5701	QY	CCTTCCAGGAGGAGGACGTTGTCTGTGAGAAATCTACCGTGTCTTCTGCTTTGGCG	5760
5701	DB	CCTTCCAGGAGGAGGACGTTGTCTGTGAGAAATCTACCGTGTCTTCTGCTTTGGCG	5760
5761	QY	GAGCTGCGCAAAAGACCTTTCGGAGGTCGGAATCTGTGGCCGTTCGACAGCGGCACGGCA	5820
5761	DB	GAGCTGCGCAAAAGACCTTTCGGAGGTCGGAATCTGTGGCCGTTCGACAGCGGCACGGCA	5820
5821	QY	ACGGCTCTCTTACACAGCCCTCCGACGAGCGGACGCGGGATTCGAGTTGAGTGTGTAC	5880
5821	DB	ACGGCTCTCTTACACAGCCCTCCGACGAGCGGACGCGGGATTCGAGTTGAGTGTGTAC	5880
5881	QY	TCCTCCATGCCCCCTTTGAGGGGACCGGGGATCCCGATCTCAGCGACCGGCTTTGG	5940
5881	DB	TCCTCCATGCCCCCTTTGAGGGGACCGGGGATCCCGATCTCAGCGACCGGCTTTGG	5940
5941	QY	TCTACCGTAAAGGAGGAGGCTAGTAGGAGCGTCTGTCTGTCTCGATGTCTTACATGG	6000
5941	DB	TCTACCGTAAAGGAGGAGGCTAGTAGGAGCGTCTGTCTGTCTCGATGTCTTACATGG	6000
6001	QY	ACAGGCGCCTGATACGCCATCGGCTGCGGAGGAACCAAGCTGCCATCAATGCATG	6060
6001	DB	ACAGGCGCCTGATACGCCATCGGCTGCGGAGGAACCAAGCTGCCATCAATGCATG	6060

Qy	6061	AGCAACTCTTTTGTCTCCGTCACCAAACTTGGTCTATGCTCAACCATCTCGCAGCGCAAGC	6120
Db	6061	AGCAACTCTTTTGTCTCCGTCACCAAACTTGGTCTATGCTCAACCATCTCGCAGCGCAAGC	6120
Qy	6121	CTGGCGCAGAAGAGGTTCACCTTTGACAGACTCGAGTCTCTGGACGACCACTACCGGGAC	6180
Db	6121	CTGGCGCAGAAGAGGTTCACCTTTGACAGACTCGAGTCTCTGGACGACCACTACCGGGAC	6180
Qy	6181	GTGCTCAAGGAGATGAAGGGGAAAGCCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAG	6240
Db	6181	GTGCTCAAGGAGATGAAGGGGAAAGCCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAG	6240
Qy	6241	GAAGCTGTAAAGCTGACGCCGCCACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAAG	6300
Db	6241	GAAGCTGTAAAGCTGACGCCGCCACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAAG	6300
Qy	6301	GACGTCGGGACCTATCCAGCAAGGCCGTTAAACCAATCCGCTCCGTGTGGAAAGGACTTG	6360
Db	6301	GACGTCGGGACCTATCCAGCAAGGCCGTTAAACCAATCCGCTCCGTGTGGAAAGGACTTG	6360
Qy	6361	CTGGAAGACACTGAGACACCAATTTGACACCAACCATCATGSCAAAATAAGGTTTCTGC	6420
Db	6361	CTGGAAGACACTGAGACACCAATTTGACACCAACCATCATGSCAAAATAAGGTTTCTGC	6420
Qy	6421	GTCCAAACGAGAGAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTTCCAGATTTGGGG	6480
Db	6421	GTCCAAACGAGAGAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTTCCAGATTTGGGG	6480
Qy	6481	GTTTCGTGTGCGAGAAATTTGGCCCTTTACGATGTGGTCTCCACCTCCCTCAGGCCGTG	6540
Db	6481	GTTTCGTGTGCGAGAAATTTGGCCCTTTACGATGTGGTCTCCACCTCCCTCAGGCCGTG	6540
Qy	6541	ATGGGCTCTTTCATACGGATTTCCAATACTCTCTCGGACAGCGGTCAGTTCCTCGTGTAAT	6600
Db	6541	ATGGGCTCTTTCATACGGATTTCCAATACTCTCTCGGACAGCGGTCAGTTCCTCGTGTAAT	6600
Qy	6601	GCCTGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCGCTGTTTGACTCA	6660
Db	6601	GCCTGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCGCTGTTTGACTCA	6660
Qy	6661	ACGGTCACTCAGAAATGACATCCGTTGTGAGGATCAATCTACCAATGTTGTGACTTGGCC	6720
Db	6661	ACGGTCACTCAGAAATGACATCCGTTGTGAGGATCAATCTACCAATGTTGTGACTTGGCC	6720
Qy	6721	CCGGAAGCCAGACAGCCATAAGGTTCGCTCAGAGAGCGCTTTACATCGGGGCCCCCTG	6780
Db	6721	CCGGAAGCCAGACAGCCATAAGGTTCGCTCAGAGAGCGCTTTACATCGGGGCCCCCTG	6780
Qy	6781	ACTAAATCTAAAGGGCAGAACTCGCGGCTATCGCCGGTCGCGCGCAGCGGTGTACTGACG	6840
Db	6781	ACTAAATCTAAAGGGCAGAACTCGCGGCTATCGCCGGTCGCGCGCAGCGGTGTACTGACG	6840
Qy	6841	ACGAGTCGGTAATACCCCTCAGATGTTACTTGAAGGCCGCTCGCGCCTGTGAGCTGCG	6900
Db	6841	ACGAGTCGGTAATACCCCTCAGATGTTACTTGAAGGCCGCTCGCGCCTGTGAGCTGCG	6900
Qy	6901	AAGCTCCGAGCTGCAGATGCTCGTATCGGAGAGGACCTTGTGTTATCTGTGAAGC	6960
Db	6901	AAGCTCCGAGCTGCAGATGCTCGTATCGGAGAGGACCTTGTGTTATCTGTGAAGC	6960
Qy	6961	GCGGGACCCAAAGAGAGCAGGCGAGCCCTACGGGCCCTTCACGAGAGCTATGACTAGATAC	7020
Db	6961	GCGGGACCCAAAGAGAGCAGGCGAGCCCTACGGGCCCTTCACGAGAGCTATGACTAGATAC	7020
Qy	7021	TTTGCCCCCTTGGGACCCGCCAAAACAGAAATACGACTTGGAGTTGATAACATCATGC	7080
Db	7021	TTTGCCCCCTTGGGACCCGCCAAAACAGAAATACGACTTGGAGTTGATAACATCATGC	7080
Qy	7081	TCTTCCAAATGTCAGTCGCGCAGCATGCTATCGGCAAAAGGTTGTAATCTCATCCGT	7140
Db	7081	TCTTCCAAATGTCAGTCGCGCAGCATGCTATCGGCAAAAGGTTGTAATCTCATCCGT	7140

Qy	7141	GA	CC	CA	CA	CA	CC	CC	CC	CT	TG	CG	GG	GG	CT	GT	GG	G	A	G	A	C	A	C	T	A	G	A	C	A	C	A	C	T	C	A	G	T	C	A	A	T	7200
Db	7141	GA	CC	CA	CA	CA	CC	CC	CC	CT	TG	CG	GG	GG	CT	GT	GG	G	A	G	A	C	A	C	T	A	G	A	C	A	C	A	C	T	C	A	G	T	C	A	A	T	7200
Qy	7201	T	C	T	G	G	C	T	A	G	G	C	C	A	C	A	T	C	A	T	G	T	G	G	C	C	A	C	C	T	T	G	G	G	C	A	A	G	A	G	A	T	7260
Db	7201	T	C	T	G	G	C	T	A	G	G	C	C	A	C	A	T	C	A	T	G	T	G	G	C	C	A	C	C	U	T	T	G	G	G	C	A	A	G	A	T	7260	
Qy	7261	A	C	T	C	A	T	T	T	C	T	C	C	A	T	T	C	T	A	G	C	T	C	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	7320
Db	7261	A	C	T	C	A	T	T	T	C	T	C	C	A	T	T	C	T	A	G	C	T	C	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	7320	
Qy	7321	A	T	C	T	A	C	G	G	G	C	T	G	T	T	A	C	T	C	A	T	T	G	A	C	C	A	C	T	T	G	A	C	T	C	A	T	C	A	T	C	A	7380
Db	7321	A	T	C	T	A	C	G	G	G	C	T	G	T	T	A	C	T	C	A	T	T	G	A	C	C	A	C	T	T	G	A	C	T	C	A	T	C	A	T	C	A	7380
Qy	7381	C	A	T	G	G	C	T	A	G	C	A	T	T	T	C	A	C	T	C	C	A	T	A	G	A	T	T	A	T	T	A	T	T	A	T	T	A	T	A	T	A	7440
Db	7381	C	A	T	G	G	C	T	A	G	C	A	T	T	T	C	A	C	T	C	C	A	T	A	G	A	T	T	A	T	T	A	T	T	A	T	T	A	T	A	T	A	7440
Qy	7441	T	C	A	T	G	C	T	A	G	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	7500	
Db	7441	T	C	A	T	G	C	T	A	G	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	7500	
Qy	7501	G	T	C	G	C	C	T	A	G	G	T	A	C	T	G	T	C	C	A	G	G	G	G	G	A	G	G	C	T	C	C	A	T	T	G	T	G	A	A	T	7560	
Db	7501	G	T	C	G	C	C	T	A	G	G	T	A	C	T	G	T	C	C	A	G	G	G	G	G	A	G	G	C	T	C	C	A	T	T	G	T	G	A	A	T	7560	
Qy	7561	A	A	C	T	G	G	C	A	G	A	C	C	A	A	G	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	7620	
Db	7561	A	A	C	T	G	G	C	A	G	A	C	C	A	A	G	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	7620	
Qy	7621	T	T	A	T	C	A	G	C	T	G	G	T	T	C	G	T	T	A	C	A	G	G	G	G	G	A	C	A	T	A	T	A	C	A	C	C	T	G	T	C	7680	
Db	7621	T	T	A	T	C	A	G	C	T	G	G	T	T	C	G	T	T	A	C	A	G	G	G	G																		

RESULT 13

RESUL I
AAL47280

AAL4/280
ID AAL47280 standard; DNA; 7992 BP.

XX
ID AAL4 / 280

AC AAL47280:

AC
XX
AAL4/280;XX
DT
30-AUG-2003 (first entry)

DT 30-AUG-2002 (first entry)
XX

XX
DE
Hepatitis C virus sub-genomic replicon recombinant clone HCVR22.

DE
XX
Hepatitis C virus sub-genomic repeat recombinant clone HCV-22.

XX
XW
Hepatitis. HCV. core-neo: NS3 proteinase/helicase: vaccine: diagnosis;

KW Hepatitis; HCV; core-neo; NS3 protease/hecticase; vaccine; diagnosis;
KW viricide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX	Hepatitis C virus.
OS	
XX	WO200238793-A2.
PN	
XX	16-MAY-2002.
PD	
XX	
XX	02-NOV-2001; 2001WO-US046350.
PF	
XX	
XX	07-NOV-2000; 2000US-0245866P.
PR	
XX	(ANAD-) ANADYS PHARM INC.
PA	
XX	Bichko V;
PI	
PT	WPI; 2002-490082/52.
DR	
XX	
XX	Novel nucleic acid encoding replication competent recombinant hepatitis C
PT	virus genome useful for screening anti-hepatitis C virus therapeutics and
PT	for vaccine development.
PT	
XX	
XX	Claim 10; Page 66-70; 85pp; English.
PS	
XX	
CC	The present invention provides protein and coding sequences from
CC	Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC	able to replicate efficiently when transfected into a susceptible cell
CC	line without reducing the growth rate of the cell line by more than 10
CC	fold. The sequences are useful for screening for anti-HCV therapeutics,
CC	for detecting antibodies to HCV in a biological sample such as blood,
CC	serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC	for deriving authentic HCV components such as replication-complement non-
CC	infectious, replication-defective infection-component, and replication-
CC	defective non-infectious HCV, in gene therapy or gene vaccination
CC	targeted to hepatic tissue for treating an animal infected or susceptible
CC	to HCV infection and for studying HCV infection and propagation. The
CC	present sequence is a clone of a fragment of the HCV genome designated
CC	HCVR22
XX	
SO	Sequence 7992 BP; 1646 A; 2368 C; 2245 G; 1733 T; 0 U; 0 Other;

Query Match	Score 7980.8;	DB 6;	Length 7992;
Best Local Similarity	99.9%;	Pred. NO. 0;	
Matches 7985: Conservative	0: Mismatches	7: Indels	0: Gaps

61 TCTTCACGCAGAAAGCGCTAGCCATGGCGTTAGTATGATGTGCGTGCAGCCTCCAGGAC 120

121 CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAA CCGGTAGTACACCGGAATTGCCAG 180

QY	181	GACGACCGGTCCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGCGTGCGCCCC	240
SH	181	GACGACCGGTCCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGCGTGCGCCCC	240

QY	241	GC	GAG	CTG	CTAG	CGC	GAG	TAG	TGT	GGG	TCC	GAA	GGC	CTT	TGG	TAT	CGT	ATG	CGC	CTG	ATAG	300
nb	241	GC	GAC	CTG	CTAG	CGC	GAG	TAG	TGT	GGG	TCC	GAA	GGC	CTT	TGG	TAT	CGT	ATG	CGC	CTG	ATAG	300

QY	301	GTGCTTGGAGTGTCCTCCCGGAGGCTTCGTAGACCGTGCCACATGAGCAGCAATCTCTAAAC	360
Nb	301	GTGCTTGGAGTGTCCTCCCGGAGGCTTCGTAGACCGTGCCACATGAGCAGCAATCTCTAAAC	360

Qy	361	CTCAAAGAAAAACCAAAAGGGCGGCCATGATTGAACAAAGATGGATTGCACGCAGGTTCTC	420
Nb	361	CTCAAAGAAAAACCAAAAGGGCGGCCATGATTGAACAAAGATGGATTGCACGCAGGTTCTC	420

QY 421 CGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCACAACAGACAATCGGCTGCT 480

Db 421 |||||CGGCCGCTGGGTGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGCTGCT 480
QY 481 CTGATGCGCCCGTGTTCGGCTGTGAGCGAGCGGGGGCCCGTCTCTTTTGTCAAGACGG 540
Db 481 CTGATGCGCCCGTGTTCGGCTGTGAGCGAGCGGGGGCCCGTCTCTTTTGTCAAGACGG 540
QY 541 ACTGTGCGGTGCCCTGAATGAATGACAGGAGCGAGCGCGGCTATCGTGGCTGGCCA 600
Db 541 ACTGTGCGGTGCCCTGAATGAATGACAGGAGCGAGCGCGGCTATCGTGGCTGGCCA 600
QY 601 CGACGGGCGTCTCTTTGCGAGCTGTGCTCGAGCTTGTCACTGAAGCGGGAAGGACTGCG 660
Db 601 CGACGGGCGTCTCTTTGCGAGCTGTGCTCGAGCTTGTCACTGAAGCGGGAAGGACTGCG 660
QY 661 TGCTATTGGGCGAAGTGGCGGGGAGGATCTCCTGTCTCATCTCCTGCTGCTGCGGAGA 720
Db 661 TGCTATTGGGCGAAGTGGCGGGGAGGATCTCCTGTCTCATCTCCTGCTGCTGCGGAGA 720
QY 721 AAGTATCCATCATGTGCTGATGCAATGCGCGGCTGCATACGCTTGCATCGGCTACCTGCC 780
Db 721 AAGTATCCATCATGTGCTGATGCAATGCGCGGCTGCATACGCTTGCATCGGCTACCTGCC 780
QY 781 CATTCGACCCACAACGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTC 840
Db 781 CATTCGACCCACAACGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTC 840
QY 841 TTGTGATCAGGATGATCTGAGCGAAGAGCATCAGGGGTGCGGCGACGCGAATGTTTCG 900
Db 841 TTGTGATCAGGATGATCTGAGCGAAGAGCATCAGGGGTGCGGCGACGCGAATGTTTCG 900
QY 901 CCAGGCTCAAGCGCGCATGCCGAGCGGAGATCTCGTGTGACCCATGGCGATGCTT 960
Db 901 CCAGGCTCAAGCGCGCATGCCGAGCGGAGATCTCGTGTGACCCATGGCGATGCTT 960
QY 961 GCTTGCAGATATCATGTTGGAAATGCGCGCTTTCTGGAATCATCGACTGTGCGCGCG 1020
Db 961 GCTTGCAGATATCATGTTGGAAATGCGCGCTTTCTGGAATCATCGACTGTGCGCGCG 1020
QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGGCTTGGCTACCGGTGATATTGCTGAAGAC 1080
Db 1021 TGGGTGTGCGGACCGCTATCAGGACATAGGCTTGGCTACCGGTGATATTGCTGAAGAC 1080
QY 1081 TTGCGCGGATGAGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTCG 1140
Db 1081 TTGCGCGGATGAGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTCG 1140
QY 1141 AGCGATGCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGATGCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGGCCCTCTCCCTCCCGCCCTTAAGTTACTGGC 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGGCCCTCTCCCTCCCGCCCTTAAGTTACTGGC 1260
QY 1261 CGAAGCGCTTGAATAAGCGGTGCTGCTGCTATATGTTATTTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGAATAAGCGGTGCTGCTGCTATATGTTATTTTCCACCATATG 1320
QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGSCCTCTCTTCTTGAAGCATTCCT 1380
Db 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGSCCTCTCTTCTTGAAGCATTCCT 1380
QY 1381 AGGGGTCTTTCCCTCTCGCAAGGAATGCAAGTCTGTTGAAATGCTGTAAGAGCA 1440
Db 1381 AGGGGTCTTTCCCTCTCGCAAGGAATGCAAGTCTGTTGAAATGCTGTAAGAGCA 1440
QY 1441 GTTCTCTGGAAGTCTTTGAAGACAAACAGCTCTGTAGGACCTTTGAGCAGCGG 1500
Db 1441 GTTCTCTGGAAGTCTTTGAAGACAAACAGCTCTGTAGGACCTTTGAGCAGCGG 1500
QY 1501 AACCCCGCACCTGGCGACAGGTGCTCTGCGGCCAAAAGCCACGCTGTATAAGATACACT 1560

Db 1501 AACCCCGCACCTGGCGACAGGTGCTCTGCGGCCAAAAGCCACGTTGTAAGATACACT 1560
QY 1561 GCAAGGCGGCAACAACCCAGTGCACGTTGTGATGTGATAGTTGTGAAAGAGTCAAA 1620
Db 1561 GCAAGGCGGCAACAACCCAGTGCACGTTGTGATGTGATAGTTGTGAAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCACAAGGGGTGAGGATGCCAGAAAGTACCCATGTT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCACAAGGGGTGAGGATGCCAGAAAGTACCCATGTT 1680
QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTGTTAGTTCGAGGTTAAAA 1740
Db 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTGTTAGTTCGAGGTTAAAA 1740
QY 1741 AACGTCTAGGCGCCCGCAACCAAGGGAGCTGGTTTCTTTGAAAAACAAGATATACC 1800
Db 1741 AACGTCTAGGCGCCCGCAACCAAGGGAGCTGGTTTCTTTGAAAAACAAGATATACC 1800
QY 1801 ATGGCGCTATTAAGGCGCTACTCCCAACAGAGCGGAGGCTACTTGGCTGCATCACT 1860
Db 1801 ATGGCGCTATTAAGGCGCTACTCCCAACAGAGCGGAGGCTACTTGGCTGCATCACT 1860
QY 1861 AGCCTCACAGCGCGGACAGAAACAGGTTCGAGGGGAGGTCCAGGTGCTTCCACCGCA 1920
Db 1861 AGCCTCACAGCGCGGACAGAAACAGGTTCGAGGGGAGGTCCAGGTGCTTCCACCGCA 1920
QY 1921 ACACAATCTTCTGGCGACCTGCGTCAATGCGGTGTTGGACTGTCTATCATGTTGCC 1980
Db 1921 ACACAATCTTCTGGCGACCTGCGTCAATGCGGTGTTGGACTGTCTATCATGTTGCC 1980
QY 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCGCCCAATACCCAAATGTACACCAATGTGAC 2040
Db 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCGCCCAATACCCAAATGTACACCAATGTGAC 2040
QY 2041 CAGGACCTCTGCTGCGTGGCAAGCGCCCGCGGCGCTTCTTGACACCATGACACCTGC 2100
Db 2041 CAGGACCTCTGCTGCGTGGCAAGCGCCCGCGGCGCTTCTTGACACCATGACACCTGC 2100
QY 2101 GGAGCTCGGACCTTTACTTGGTCAAGGAGCATCCGATGTCAITTCGCTGCGCGCGG 2160
Db 2101 GGAGCTCGGACCTTTACTTGGTCAAGGAGCATCCGATGTCAITTCGCTGCGCGCGG 2160
QY 2161 GGCGACAGCGGGGAGGCTACTCTCCCGAGGCGCTTCTGAGGCTGCGGCTGCTTCG 2220
Db 2161 GGCGACAGCGGGGAGGCTACTCTCCCGAGGCGCTTCTGAGGCTGCGGCTGCTTCG 2220
QY 2221 GGCGCTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTCGCGCTGCGGCTGCTTCG 2280
Db 2221 GGCGCTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTCGCGCTGCGGCTGCTTCG 2280
QY 2281 ACCGAGGGTTCGAAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG 2340
Db 2281 ACCGAGGGTTCGAAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG 2340
QY 2341 CGGTCCCGGTTCACGCAACTCGTCCCTCGCGCGTACCGGACACTTCCAGTTCGAGTG 2400
Db 2341 CGGTCCCGGTTCACGCAACTCGTCCCTCGCGCGTACCGGACACTTCCAGTTCGAGTG 2400
QY 2401 GCCCATCTACACGCCCTTACTGTGTAGCGGCAAGACACTAAGTGCCTGCTATGCA 2460
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QY 2461 GCCCAAGGTTAAGGTGCTTCTGAAACCCGTCGCTGCGCGCAACCTAGGTTTCGG 2520
Db 2461 GCCCAAGGTTAAGGTGCTTCTGAAACCCGTCGCTGCGCGCAACCTAGGTTTCGG 2520
QY 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAGACCATC 2580
Db 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAGACCATC 2580
QY 2581 ACCACGGTTCGCCCATCAGGTACTCTCACCTATGGAAGTTCCTTCCGACGGTTCG 2640
Db 2581 ACCACGGTTCGCCCATCAGGTACTCTCACCTATGGAAGTTCCTTCCGACGGTTCG 2640

QY 301 GTGCTGCGAGTCCCCGGGAGGTCTCGTAGACCCGTGACCACTAGACAGCAATCCTAAAC 360
DB 301 GTGCTGCGAGTCCCCGGGAGGTCTCGTAGACCCGTGACCACTAGACAGCAATCCTAAAC 360
QY 361 CTCAAAGAAAACCAAAGGCGCGGCATGATTGAACAAGATGGAATGCAAGGTTCTC 420
DB 361 CTCAAAGAAAACCAAAGGCGCGGCATGATTGAACAAGATGGAATGCAAGGTTCTC 420
QY 421 CGGCGCTGCGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
DB 421 CGGCGCTGCGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
QY 481 CTGATGCGCGCTGTTCCGGCTGTGTCAGCGCAGGCGCGCCGGTCTCTTTTGTCAAGACCG 540
DB 481 CTGATGCGCGCTGTTCCGGCTGTGTCAGCGCAGGCGCGCCGGTCTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCGGTGCCTGTAATGAACTGCAAGGAGGCGCGGCTATGCTGGCTGGGCA 600
DB 541 ACCTGTCGGTGCCTGTAATGAACTGCAAGGAGGCGCGGCTATGCTGGCTGGGCA 600
QY 601 CGAACGGCGTCTCTTGGCGAGCTGTGCTCGAGCTGTGCTCACTGAAGCGGGAAGGACTGGC 660
DB 601 CGAACGGCGTCTCTTGGCGAGCTGTGCTCGAGCTGTGCTCACTGAAGCGGGAAGGACTGGC 660
QY 661 TGCTATTGGGGAAGTCCGGGCGAGGATCTCTGTCATCTCACCTGTCTCTGCGCGAGA 720
DB 661 TGCTATTGGGGAAGTCCGGGCGAGGATCTCTGTCATCTCACCTGTCTCTGCGCGAGA 720
QY 721 AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATAGCGTTGATCCGGCTACCTGCC 780
DB 721 AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATAGCGTTGATCCGGCTACCTGCC 780
QY 781 CATTCGACCAACCAAGCGAAACATCCATCGAGCGAGCAGCTACTCGGATGGAAGCGGTC 840
DB 781 CATTCGACCAACCAAGCGAAACATCCATCGAGCGAGCAGCTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGGATGATCTGACGAGAGCATCAGGGGCTCGCGCAGCGCAACTGTTTCG 900
DB 841 TTGTGATCAGGATGATCTGACGAGAGCATCAGGGGCTCGCGCAGCGCAACTGTTTCG 900
QY 901 CCAGGCTCAAGCGCGGATGCCGAGCGGAGGATCTCGTGTGACCCCATGCGGATGCC 960
DB 901 CCAGGCTCAAGCGCGGATGCCGAGCGGAGGATCTCGTGTGACCCCATGCGGATGCC 960
QY 961 GCTTGGCGAATATCATGCTGGAATAATGCCCTTTCTGGATTTCAGCTGTGGCGGCG 1020
DB 961 GCTTGGCGAATATCATGCTGGAATAATGCCCTTTCTGGATTTCAGCTGTGGCGGCG 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC 1080
DB 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGAGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
DB 1081 TTGGCGGGAATGAGCTGACCGCTTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTTTAAACAGACCACAAGC 1200
DB 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTTTAAACAGACCACAAGC 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCTCCCTCCCGCCCTTAAGCTTACTGGC 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCTCTCCCTCCCGCCCTTAAGCTTACTGGC 1260
QY 1261 CGAAGCGCTTGAATAGGCGGCTGCGTTGCTATATGTTATTTTCCACCATATTG 1320
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DB 1321 CCGTCTTTTGGCAATGTAGGCGCGCGAAACCTCGCCCTGTCTTGTGAGGAGCAATTCCT 1380
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DB 1381 AGGGGTCTTTCCCTCTCGCGAAAGGAATGCAAGGCTCTGTTGAATGCTGAAGGAAGCA 1440
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DB 1441 GTTCTCTGGAAGCTTTCTTGAAGACAAACAGTCTGTAGCGACCTTTTGCAGGCGAGCG 1500
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DB 1501 AACCCCGCACTGCGGACAGAGTCTCTGCGGCCAAAAGCCACGTTGTAAGATACACCT 1560
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DB 1741 AACGCTAGGCGCCCGGAAACCAACCGGAGCTGCTTTTCTTTGAAAACACAGATATACC 1800
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DB 1801 ATGGCGCTATTAGCGCTACTTCCCAACAGAGCGGAGGCTACTTGGCTGCAATCACT 1860
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DB 1861 AGCCTCACAGGCGGGAACAGGAAACAGGTCGAGGGGAGGTCAGGTCCTCCACCGCA 1920
QY 1921 ACACAATCTTCTCTGGGACCTGCTCAATGCGCTGTGTTGCACTGTATCATGCTGCC 1980
DB 1921 ACACAATCTTCTCTGGGACCTGCTCAATGCGCTGTGTTGCACTGTATCATGCTGCC 1980
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DB 1981 GGCTCAAGAGCCTTGGCGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
QY 2041 CAGAACCTGCTGCGCTGGAAGCGCCCGCGGGGCGGTCCTTTGACACCATGCACTGCG 2100
DB 2041 CAGAACCTGCTGCGCTGGAAGCGCCCGCGGGGCGGTCCTTTGACACCATGCACTGCG 2100
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DB 2101 GGCACTCGGACCTTTACTTGTGTCAGGAGCATGCGGATGTCATTCGGTGGCGGCGG 2160
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DB 2281 ACCCGAGGGGTGCGAAGGCGGTGGACTTTGTACCGCTCGAGTCTATGGAACACCATATG 2340
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DB 2341 CCGTCCCGGTCTTTCACGGAACCTCGTCCCTCCGCGCGTACCGCAGACATTCAGGAG 2400
QY 2401 GCCCATCTACCGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460
DB 2401 GCCCATCTACCGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460
QY 2461 GCCCAAGGGTATAGGTGCTTGTCTGAACCCCTCGTGGCGCCGACCTTAGGTTTCGG 2520

2461 GCCAAGGGTATAAGGTGCTTCTGCTGTAACCCGTCGGTCGGCCGACCCCTAGGTTTCGGG 2520 Db
2521 GCGTATATCTAAGGCAATGGTATCGACCTTAACATCAGAAACCGGGGTAAAGGACATC 2580 QY
2521 GCGTATGTTCTAAGGCAATGGTATCGACCCCTAAACATCAGAAACCGGGGTAAAGGACATC 2580 Db
2581 ACCACGGGTGCCCCCATCAGCTACTCCACCTATGGCAAGTTTCTGCCGACGGTGGTTCG 2640 QY
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2641 TCTGGGGGCGCTATCAGCATCATATATGTGTAGTGCCACTCAACTGACTCGACCACT 2700 QY
2641 TCTGGGGGCGCTATGACATCATATATGTGTAGTGCCACTCAACTGACTCGACCACT 2700 Db
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2941 AAGCTGTCGGCTCGGACTCAATGTGTAGCATATTCACGGGCGCTTGATGTATCCGTC 3000 Db
3001 ATACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTACC 3060 QY
3001 ATACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTACC 3060 Db
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3181 CAGCGGCGAGCGAGCTGTTAGGGGAGGATGGGCATTTACAGTTTGTGACTCCAGGA 3240 QY
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3361 CCAAGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTC 3420 QY
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3421 ACCCATAGACCGCATTTCTGTCAGACTAAGCAGGCGAGAGCACTTCCCTTAC 3480 QY
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3481 CTGTTAGCATACAGGCTACGGTGTGGCCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540 QY
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3541 CAATGTGGAAGTGTCTCATACGGCTAAGCTACGCTGACGGGCGCAACGCCCTGCTG 3600 QY
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3601 TATAGCTGGAGCCGTTCAAACGAGGTTACTACACACACCCCATACCAATACATC 3660 QY
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3721 GTCTTAGAGCTCTGGCCGCGTATTCCTGCAACAGGCGAGGTCATTTGCGGAGG 3780 QY
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3781 ATCATCTTCTCGGAAGGCGCCATCATTTCCCGACAGGGAAGTCCCTTACCGGGAGTTC 3840 QY
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3901 GAACAATTCAGACAGAGGCAATCGGTTGCTGCAACAGGCGACCAAGCAAGCGGAGGCT 3960 QY
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3961 GCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCCCTCGAAGCCCTTCTGGGCGAAGCATATG 4020 QY
3961 GCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCCCTCGAAGCCCTTCTGGGCGAAGCATATG 4020 Db
4021 TGGAAATTCATCAGCGGATACAAATATTTAGCAGGCTTGTCTCACTCTGCTGCGCAACCCC 4080 QY
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4081 GCGATAGCATCACTGATGGCAATTCACAGCTCTATCAGAGCCGCTCACCACCCCAACAT 4140 QY
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4201 GCTTCTGCTTTGATGAGCGCGGATCGCTGAGAGCGGCTGTTGGCAGCATAGGCTTGGG 4260 QY
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4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGAGAGCAGGGTGGCAGCGCGCTCGTGCC 4320 QY
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4381 ATCTCTCCCTCGGCGGCTTGTGCTGGGTCGTGTCGAGGATCTGCGTTCGCGG 4440 QY
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4441 GTGGGCGGAGGAGGCGGCTGTGCTAGTGAACCGGCTGATGAGGCTTGGCTTCGCGG 4500 QY
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4561 CAGATCTCTCTAGTCTTACCATCAGTCTGAGAGGCTTCCACGAGTGCATCAAC 4620 QY
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4621 GAGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGATATGC 4680 QY
4621 GAGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGATATGC 4680 Db

Qy	4681	ACGGTGTGATGATATTTCAAGACCTTGGCTCCAGTCCAAAGCTCTTGC CGCGAATTC CGCGGA	4740
Db	4681	ACGGTGTGACTGATATTTCAAGACCTTGGCTCCAGTCCAAAGCTCTTGC CGCGAATTC CGCGGA	4740
Qy	4741	GTCCCTCTTCTCTCATGTCAAGTGGGTACAAAGGAGTCTTGGCGGGGCGACGGCATCATG	4800
Db	4741	GTCCCTCTTCTCTCATGTCAAGTGGGTACAAAGGAGTCTTGGCGGGGCGACGGCATCATG	4800
Qy	4801	CAAAACCACTCTCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAGGTTTCCATCAGG	4860
Db	4801	CAAAACCACTCTCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAGGTTTCCATCAGG	4860
Qy	4861	ATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGGATGAAACATTTCCCCATTTAACCGGTAC	4920
Db	4861	ATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGGATGAAACATTTCCCCATTTAACCGGTAC	4920
Qy	4921	ACCAAGGCGCCCTGCAGCGCCCTCCCGCGCGCAATTTATTTCTAGGCGCTGTGCGCGGCTG	4980
Db	4921	ACCAAGGCGCCCTGCAGCGCCCTCCCGCGCGCAATTTATTTCTAGGCGCTGTGCGCGGCTG	4980
Qy	4981	GCTGCTGAGGAGTAGTGGAGGTTTACCGCGGTGGGGGATTTTCCACTACGTGACGGGCATG	5040
Db	4981	GCTGCTGAGGAGTAGTGGAGGTTTACCGCGGTGGGGGATTTTCCACTACGTGACGGGCATG	5040
Qy	5041	ACCACTGACACGTAAGTGCCCGTGTCAAGTTTCCGCGCCCGGAATTTCTTCAAGAAAGTG	5100
Db	5041	ACCACTGACACGTAAGTGCCCGTGTCAAGTTTCCGCGCCCGGAATTTCTTCAAGAAAGTG	5100
Qy	5101	GATGGGTGGGTTGACACAGTAGCTCCAGCGTGGCAACCCCTCTTACGGGAGGAGTTC	5160
Db	5101	GATGGGTGGGTTGACACAGTAGCTCCAGCGTGGCAACCCCTCTTACGGGAGGAGTTC	5160
Qy	5161	ACAATTCCTGGTTCGGGCTCAATCAATACCTGTGTGGGTACAGTCTCCCATCGGAGCCGAA	5220
Db	5161	ACAATTCCTGGTTCGGGCTCAATCAATACCTGTGTGGGTACAGTCTCCCATCGGAGCCGAA	5220
Qy	5221	CCGACGCTAGAGTGTCACTTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGACG	5280
Db	5221	CCGACGCTAGAGTGTCACTTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGACG	5280
Qy	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCGAGTCTCATCGTACGCGAG	5340
Db	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCGAGTCTCATCGTACGCGAG	5340
Qy	5341	CTGTCTCGGCTTCTTCTTGAAGGCAACATGCACTACCCGTCACTACCTCCCGGACGCTGAC	5400
Db	5341	CTGTCTCGGCTTCTTCTTGAAGGCAACATGCACTACCCGTCACTACCTCCCGGACGCTGAC	5400
Qy	5401	CTCATTCAGGCGCAACCTCTCTGTGGCGCAGGAGATGGGCGGGAACATCAACCCGCTGGAG	5460
Db	5401	CTCATTCAGGCGCAACCTCTCTGTGGCGCAGGAGATGGGCGGGAACATCAACCCGCTGGAG	5460
Qy	5461	TCAGAAAAAAGGTAGTAAATTTTGGACTTTTCGAGCGCTTCAAGCGGAGGAGGATGAG	5520
Db	5461	TCAGAAAAAAGGTAGTAAATTTTGGACTTTTCGAGCGCTTCAAGCGGAGGAGGATGAG	5520
Qy	5521	AGGGAAGTATCCGTTCCGGCGGAGATCCTTCGGAGGTCAGGAAAAATTTCCCTTCAGCGATG	5580
Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCCTTCGGAGGTCAGGAAAAATTTCCCTTCAGCGATG	5580
Qy	5581	CCCATATGGGCAAGCGGAGTTCATTCGCGGCTTCCCAAGCGGCCCTTCGATACCA	5640
Db	5581	CCCATATGGGCAAGCGGAGTTCATTCGCGGCTTCCCAAGCGGCCCTTCGATACCA	5640
Qy	5641	TAGTCTCCCTCCAGTGGTACACGGGTGTCCATTCGCGGCTTCCCAAGCGGCCCTTCGATACCA	5700
Db	5641	TAGTCTCCCTCCAGTGGTACACGGGTGTCCATTCGCGGCTTCCCAAGCGGCCCTTCGATACCA	5700
Qy	5701	CCTCCACGGAGGAAGGACGGTTGTCTGTCAAGATCTTACCGTGTCTTCTGCTTGGCG	5760
Db	5701	CCTCCACGGAGGAAGGACGGTTGTCTGTCAAGATCTTACCGTGTCTTCTGCTTGGCG	5760
Qy	5761	GAGTCTGCCACAAAGACTTTTCGGCAGCTCCGAATCTGTCGGCCGCTCGACACGGGCACGCA	5820

Db	5761		GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAATCTGTGCGCCGTGACAGCGCACCGCA	5820
Qy	5821	ACGGCCTCTCTGTACACAGCCCTTCGACGACGCGACCGGATCCGACGTTGAGTCGTAC	5880	
Db	5821	ACGGCCTCTCTGTACACAGCCCTTCGACGACGCGACCGGATCCGACGTTGAGTCGTAC	5880	
Qy	5881	TCCTCATGCCCCCTTTGAGGGGAGCGCGGGATCCGATCTCAGCAGCGGTCTTTGG	5940	
Db	5881	TCCTCATGCCCCCTTTGAGGGGAGCGCGGGATCCGATCTCAGCAGCGGTCTTTGG	5940	
Qy	5941	TCTACCGTAAGCAGAGGCTTAGTGAGGACGTCTGCTCTGCTCGATGTCTTACACATGG	6000	
Db	5941	TCTACCGTAAGCAGAGGCTTAGTGAGGACGTCTGCTCTGCTCGATGTCTTACACATGG	6000	
Qy	6001	ACAGCGCCCTGTATCAGCCATGCGCTGCGAGGAAACCAAGCTGCCATCAATGACACTG	6060	
Db	6001	ACAGCGCCCTGTATCAGCCATGCGCTGCGAGGAAACCAAGCTGCCATCAATGACACTG	6060	
Qy	6061	AGCAACTCTTTGCTCCGTCACCAACTTTGGTCTATGTCTACACATCTCGAGCGCAAGC	6120	
Db	6061	AGCAACTCTTTGCTCCGTCACCAACTTTGGTCTATGTCTACCACTCTCGAGCGCAAGC	6120	
Qy	6121	CTGGCGCAGAGAAAGCTCACCTTTGACAGACTGCAAGTCTCTGACGACCACCTACCGGAC	6180	
Db	6121	CTGGCGCAGAGAAAGCTCACCTTTGACAGACTGCAAGTCTCTGACGACCACCTACCGGAC	6180	
Qy	6181	GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTTAAGGCTAAAGCTTATCCGTGGAG	6240	
Db	6181	GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTTAAGGCTAAAGCTTATCCGTGGAG	6240	
Qy	6241	GAAGCCTGTAAGCTGAGCGCCCCACATTTGGCCAGATCTAAATTTGGCTATGGGCAAG	6300	
Db	6241	GAAGCCTGTAAGCTGAGCGCCCCACATTTGGCCAGATCTAAATTTGGCTATGGGCAAG	6300	
Qy	6301	GACGTCGCGAACCTATCCAGCAAGCGCGTTAAACCATCGCTCCGCTGTGGAGGACTTG	6360	
Db	6301	GACGTCGCGAACCTATCCAGCAAGCGCGTTAAACCATCGCTCCGCTGTGGAGGACTTG	6360	
Qy	6361	CTGGAAGACACTGAGACACCAATTGACACCAACCATATGGCAAAAAATAGGTTTTCTGC	6420	
Db	6361	CTGGAAGACACTGAGACACCAATTGACACCAACCATATGGCAAAAAATAGGTTTTCTGC	6420	
Qy	6421	GTCCACACGAGAGGGGCGCCAGACCAAGCTCGCTTATCGTATTTCCAGATTTGGGG	6480	
Db	6421	GTCCACACGAGAGGGGCGCCAGACCAAGCTCGCTTATCGTATTTCCAGATTTGGGG	6480	
Qy	6481	GTTTCGTGTGTGCGAGAAAAATGGCCCTTTACGATGTGCTCTCCACCCCTCCCTCAGGCCGTG	6540	
Db	6481	GTTTCGTGTGTGCGAGAAAAATGGCCCTTTACGATGTGCTCTCCACCCCTCCCTCAGGCCGTG	6540	
Qy	6541	ATGGGCTCTTCAATACGGAATTCAAATCTCTCTGGACAGCGGTTCGAGTTCTGTGTAAT	6600	
Db	6541	ATGGGCTCTTCAATACGGAATTCAAATCTCTCTGGACAGCGGTTCGAGTTCTGTGTAAT	6600	
Qy	6601	GCCTGGAACGGAAGAAATGCCCTATGGGCTTCGCAATGACACCGCTGTTTGACTCA	6660	
Db	6601	GCCTGGAACGGAAGAAATGCCCTATGGGCTTCGCAATGACACCGCTGTTTGACTCA	6660	
Qy	6661	ACGGTCACTGAGAAATGACATCCGTGTGAGGAGTCAATCTCAATGTTGTGACTTGGCC	6720	
Db	6661	ACGGTCACTGAGAAATGACATCCGTGTGAGGAGTCAATCTCAATGTTGTGACTTGGCC	6720	
Qy	6721	CCGAAGCCAGACAGGCCATAAGTTCGCTCAAGAGCGGCTTTACATCGGGGGCCCCCTG	6780	
Db	6721	CCGAAGCCAGACAGGCCATAAGTTCGCTCAAGAGCGGCTTTACATCGGGGGCCCCCTG	6780	
Qy	6781	ACTAAATCTTAAGGCGAGAACTGCGGCTATCCCGGTGCCGCGAGCGGTGTACTGACG	6840	
Db	6781	ACTAAATCTTAAGGCGAGAACTGCGGCTATCCCGGTGCCGCGAGCGGTGTACTGACG	6840	
Qy	6841	ACCAGCTCGGTAATAACCCCTCACTGTTTGAAGGCGGCTGCGGCTGTGAGCTGCG	6900	

QY 181 GACGACCGGGTCTTTCTTGATCAACCGCTCAATGCTGTGAGATTTTGGGGTGCCTCC 240
DB 181 GACGACCGGGTCTTTCTTGATCAACCGCTCAATGCTGTGAGATTTTGGGGTGCCTCC 240
QY 241 GCGAGACTGCTAGCGAGTAGTGTGGGTGCGAAAGCGCTTGTGCTGCTCATAGG 300
DB 241 GCGAGACTGCTAGCGAGTAGTGTGGGTGCGAAAGCGCTTGTGCTGCTCATAGG 300
QY 301 GTGCTTGGAGTGGCCCGGAGGTCTCGTAGACCTGTGACCAATGAGCAAGAACTCTAAGC 360
DB 301 GTGCTTGGAGTGGCCCGGAGGTCTCGTAGACCTGTGACCAATGAGCAAGAACTCTAAGC 360
QY 361 CTCAAAGAAAAACAAAGGCGCGCATGATTGAACAAGATGGATTGCAAGCAGGTCTTC 420
DB 361 CTCAAAGAAAAACAAAGGCGCGCATGATTGAACAAGATGGATTGCAAGCAGGTCTTC 420
QY 421 CGCGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCACAAACAGCAATCGGCTGCT 480
DB 421 CGCGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCACAAACAGCAATCGGCTGCT 480
QY 481 CTGATCGCGCGTGTTCGGCTGTGTCAGCGAGGGCGCGCGTTCCTTTTGTCAAGACCG 540
DB 481 CTGATCGCGCGTGTTCGGCTGTGTCAGCGAGGGCGCGCGTTCCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGGTGCCTGAATGAATGCAAGGACGAGGCGAGCGGCTATCGTGGCTGGCCA 600
DB 541 ACCTGTCCGGTGCCTGAATGAATGCAAGGACGAGGCGAGCGGCTATCGTGGCTGGCCA 600
QY 601 CGACGGGGTTCCTTGGCAGCTGTGTCGAGCTGTGTCACAGCGGGAAGGAGCTGGC 660
DB 601 CGACGGGGTTCCTTGGCAGCTGTGTCGAGCTGTGTCACAGCGGGAAGGAGCTGGC 660
QY 661 TGCTATTGGGCGAAGTGGCGGCGAGGATCTCGTGTGATCTCACTTGTCTCGCGAGA 720
DB 661 TGCTATTGGGCGAAGTGGCGGCGAGGATCTCGTGTGATCTCACTTGTCTCGCGAGA 720
QY 721 AAGTATCCATCATGGCTGATGCAATGGCGGCGCTGATACCTTGTATCCGGCTACCTGCC 780
DB 721 AAGTATCCATCATGGCTGATGCAATGGCGGCGCTGATACCTTGTATCCGGCTACCTGCC 780
QY 781 CATTCGACCAAGCGGAACATCGCATCGAGCGAGCACGCTACTCGGATGGAACCGGTC 840
DB 781 CATTCGACCAAGCGGAACATCGCATCGAGCGAGCACGCTACTCGGATGGAACCGGTC 840
QY 841 TTGTGATCAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCACGCGAATCTGTCG 900
DB 841 TTGTGATCAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCACGCGAATCTGTCG 900
QY 901 CCAAGGCTCAAGGGCGCATGCGCGAGGAGATCTCGTGTGACCATGCGGATCGCT 960
DB 901 CCAAGGCTCAAGGGCGCATGCGCGAGGAGATCTCGTGTGACCATGCGGATCGCT 960
QY 961 GCTTGGGAATATCATGGTGGAAATGGCGGCTTTCGATTCATCGACTGGCGCGC 1020
DB 961 GCTTGGGAATATCATGGTGGAAATGGCGGCTTTCGATTCATCGACTGGCGCGC 1020
QY 1021 TGCGGTGGCGGACCGCTATCAGGACATAGCTGGCTACCGGTGATTTGCTGAGAGC 1080
DB 1021 TGCGGTGGCGGACCGCTATCAGGACATAGCTGGCTACCGGTGATTTGCTGAGAGC 1080
QY 1081 TTGGCGGGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTTCG 1140
DB 1081 TTGGCGGGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTTCG 1140
QY 1141 AGCGCATCGCCTTCTATCGCCTTCTGAGCAAGTCTTCTGAGTTTAAACAGACCAACG 1200
DB 1141 AGCGCATCGCCTTCTATCGCCTTCTGAGCAAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTACAGTTCGCTGGC 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTACAGTTCGCTGGC 1260

QY 1261 CGAAGCCGCTTGGATTAAGCGCGTGTGGTGTCTATATCTTATTTTCCACCATATTG 1320
DB 1261 CGAAGCCGCTTGGATTAAGCGCGTGTGGTGTCTATATCTTATTTTCCACCATATTG 1319
QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTTCTTGACGAGCAATCT 1380
DB 1320 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTTCTTGACGAGCAATCT 1379
QY 1381 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAAATGTCGTGAAGGAAGCA 1440
DB 1380 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAAATGTCGTGAAGGAAGCA 1439
QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACAGCTCTGTAGCGACCTTTGACGAGCGG 1500
DB 1440 GTTCTCTGGAAGCTTCTTGAAGCAAAACAGCTCTGTAGCGACCTTTGACGAGCGG 1499
QY 1501 AACCCCGCCACCTGGCGACAGGTGCTCTCGGCCCAAAAGCCACGCTGATTAAGATACCT 1560
DB 1500 AACCCCGCCACCTGGCGACAGGTGCTCTCGGCCCAAAAGCCACGCTGATTAAGATACCT 1559
QY 1561 GCAAAGCGCGCACAAACCCAGTGCACGTTGTGAGTTGGAATGTTGTAAGAGTCAAA 1620
DB 1560 GCAAAGCGCGCACAAACCCAGTGCACGTTGTGAGTTGGAATGTTGTAAGAGTCAAA 1619
QY 1621 TGGCTCTCTCAAGGCTATTCAAACAGGGGCTGAAAGATGCCAGAGGTACCCCATTTG 1680
DB 1620 TGGCTCTCTCAAGGCTATTCAAACAGGGGCTGAAAGATGCCAGAGGTACCCCATTTG 1679
QY 1681 ATGGGATCTGATCTGGGGCTCTCGGTGCACATGCTTATCATGTGTTAGTCGAGGTAAAA 1740
DB 1680 ATGGGATCTGATCTGGGGCTCTCGGTGCACATGCTTATCATGTGTTAGTCGAGGTAAAA 1739
QY 1741 AACCTCTAGGCCCCCGAACACAGGGGACGTGGTTCCTTTGAAAAACACATAATACC 1800
DB 1740 AACCTCTAGGCCCCCGAACACAGGGGACGTGGTTCCTTTGAAAAACACATAATACC 1799
QY 1801 ATGGCGCTTATTAGGGCTACTCCCAACAGCGGAGGCTTACTTTGGCTGTCATCATCACT 1860
DB 1800 ATGGCGCTTATTAGGGCTACTCCCAACAGCGGAGGCTTACTTTGGCTGTCATCATCACT 1859
QY 1861 AGCTCTACAGCGCGGACAGGAACAGGTGAGGGGAGGTCCAGGTGCTCCACCGCA 1920
DB 1860 AGCTCTACAGCGCGGACAGGAACAGGTGAGGGGAGGTCCAGGTGCTCCACCGCA 1919
QY 1921 ACACAATCTTTCTGGCGACTCTGCTCAATGGCGTGTGTGGACTGTCTATCATGTGTC 1980
DB 1920 ACACAATCTTTCTGGCGACTCTGCTCAATGGCGTGTGTGGACTGTCTATCATGTGTC 1979
QY 1981 GGCTCAAGACCTTGGCGGCGCCAAAGGGCCCAATACCCAAATGTACCAATGTGGAC 2040
DB 1980 GGCTCAAGACCTTGGCGGCGCCAAAGGGCCCAATACCCAAATGTACCAATGTGGAC 2039
QY 2041 CAGGACTCTGCTGGCTGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGC 2100
DB 2040 CAGGACTCTGCTGGCTGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACTGC 2099
QY 2101 GGAGCTCGGACTTTTACTTGGTCAAGGATGTCGATTCCTGGTGGCGCGG 2160
DB 2100 GGAGCTCGGACTTTTACTTGGTCAAGGATGTCGATTCCTGGTGGCGCGG 2159
QY 2161 GGCGACAGGAGGGGAGCTTCTCTCCCGAGCGCTCTCTTGAAGGGCTCTTCG 2220
DB 2160 GGCGACAGGAGGGGAGCTTCTCTCCCGAGCGCTCTCTTGAAGGGCTCTTCG 2219
QY 2221 GGCGTCTCACTGCTCTGCGCTCGGGGACGCTGTGGGCTCTTTCCGGCTGCGGTGTC 2280
DB 2220 GGCGTCTCACTGCTCTGCGCTCGGGGACGCTGTGGGCTCTTTCCGGCTGCGGTGTC 2279
QY 2281 ACCGAGGGGTTGCGAAGCGGTGGAATTTGTACCGCTCGAGTCTATGGAACCACTATG 2340
DB 2280 ACCGAGGGGTTGCGAAGCGGTGGAATTTGTACCGCTCGAGTCTATGGAACCACTATG 2339
QY 2341 CGGTCCCGGTCTTTCAGGACAACTCGTCCCTCGCGCGGTACCGGACAGATTTCCAGGTG 2400

Db	2340	CGGTCCCGGCTTTACCGGCAACTCTGTCCTCCGCGCGTACCGGACATTCAGGTG	2399	Db	3420	ACCCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGGAGCAAACTTCCCTTAC	3479
Qy	2401	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCA	2460	Qy	3481	CTGGTAGCATACCAAGGCTACCGTGTGCGCCAGGGCTCAGAGGTCCACCTCCATCTGTTGGAC	3540
Db	2400	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCA	2459	Db	3480	CTGGTAGCATACCAAGGCTACCGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCTGTTGGAC	3539
Qy	2461	GCCCAAGGGTATAAGGTGTTGTCCTGAACCGTCCGTCGCGCCACACCTTAGTTTCGGG	2520	Qy	3541	CAATGTGGAAGTGTCTCATACGGGTAAAGCTTACGCTGACAGGSCAAACGCCCTTGTG	3600
Db	2460	GCCCAAGGGTATAAGGTGTTGTCCTGAACCGTCCGTCGCGCCACACCTTAGTTTCGGG	2519	Db	3540	CAATGTGGAAGTGTCTCATACGGGTAAAGCTTACGCTGACAGGSCAAACGCCCTTGTG	3599
Qy	2521	GGGTATATGTTCTAAGGCAATGGTATCGACCTTAACATCAGAACCGGGTAAAGCAATC	2580	Qy	3601	TATAGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATAAACAAATACATC	3660
Db	2520	GGGTATATGTTCTAAGGCAATGGTATCGACCTTAACATCAGAACCGGGTAAAGCAATC	2579	Db	3600	TATAGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATAAACAAATACATC	3659
Qy	2581	ACCACGGGTGCCCCCATCACTGATCTCCACCTATGGAAGTTCCTGCGACGGTGTGC	2640	Qy	3661	ATGGCATGCATGTCCTGGCTGACCTGGAGGTGCTCAGAGCACCTGGTGTGTAGCGGA	3720
Db	2580	ACCACGGGTGCCCCCATCACTGATCTCCACCTATGGAAGTTCCTGCGACGGTGTGC	2639	Db	3660	ATGGCATGCATGTCCTGGCTGACCTGGAGGTGCTCAGAGCACCTGGTGTGTAGCGGA	3719
Qy	2641	TCTGGGGGGCTATGACATCATATATGTGATGTCCTCAACTGACCTCGACCAT	2700	Qy	3721	GTCTAGCAGCTCTCGCGCGTATTTGCTGACAAACAGGAGCGTGTGTCATTTGTTGGCAG	3780
Db	2640	TCTGGGGGGCTATGACATCATATATGTGATGTCCTCAACTGACCTCGACCAT	2699	Db	3720	GTCTAGCAGCTCTCGCGCGTATTTGCTGACAAACAGGAGCGTGTGTCATTTGTTGGCAG	3779
Qy	2701	ATCTGGGCATCGGACAGTCTTGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTG	2760	Qy	3781	ATCATCTTTGTCGGGAAGCGCGCCATCATTTCCCGACAGGAAAGTCTTTTACCGGAGTTTC	3840
Db	2700	ATCTGGGCATCGGACAGTCTTGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTG	2759	Db	3780	ATCATCTTTGTCGGGAAGCGCGCCATCATTTCCCGACAGGAAAGTCTTTTACCGGAGTTTC	3839
Qy	2761	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTCCCATCAATCAAAATCGAGGAGTG	2820	Qy	3841	GATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAAACAGGAAATGACGTCTGCC	3900
Db	2760	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTCCCATCAATCAAAATCGAGGAGTG	2819	Db	3840	GATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAAACAGGAAATGACGTCTGCC	3899
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880	Qy	3901	GAACAATCAAAACAGAAAGCAATCGGGTGTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT	3960
Db	2820	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2879	Db	3900	GAACAATCAAAACAGAAAGCAATCGGGTGTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT	3959
Qy	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCCAAGAAAGTGTGATGAGCTCGCGCG	2940	Qy	3961	GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCCCTCTGGGCGAAGCATATG	4020
Db	2880	AAGGGGGGAGGAGCACTCATTTTCTGCCATTCCAAGAAAGTGTGATGAGCTCGCGCG	2939	Db	3960	GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCCCTCTGGGCGAAGCATATG	4019
Qy	2941	AAGCTCTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGATGATCGGTC	3000	Qy	4021	TGGAAATTCATCAGCGGGGATCAATAATTTAGCAGGCTTGTCCAATCTGCTGCTGCAACCCC	4080
Db	2940	AAGCTCTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGATGATCGGTC	2999	Db	4020	TGGAAATTCATCAGCGGGGATCAATAATTTAGCAGGCTTGTCCAATCTGCTGCTGCAACCCC	4079
Qy	3001	ATACCAACTAGCGGAGCGTCTGCTAGCAACGAGCGCTCTAATGACGGCTTTACC	3060	Qy	4081	GCATAGCATCATGATGGCATTCACAGCTCTATCAGCAGCGCGCTCACACCCACACAT	4140
Db	3000	ATACCAACTAGCGGAGCGTCTGCTAGCAACGAGCGCTCTAATGACGGCTTTACC	3059	Db	4080	GCATAGCATCATGATGGCATTCACAGCTCTATCAGCAGCGCGCTCACACCCACACAT	4139
Qy	3061	GGCGATTCGACTCAGTGATCGACTGCAATACATGTGTCTACCCAGACAGTCTTACG	3120	Qy	4141	ACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCT	4200
Db	3060	GGCGATTCGACTCAGTGATCGACTGCAATACATGTGTCTACCCAGACAGTCTTACG	3119	Db	4140	ACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCT	4199
Qy	3121	CTGACCCGACCTTACCATTTAGAGACGACGCTGCTGCAAGCGGCTTACCGCTCG	3180	Qy	4201	GCTTCTGCTTTCTAGCGCGGCTGCTGCTGAGAGCGGCTTGTGGAGCATAGGCTTTGGG	4260
Db	3120	CTGACCCGACCTTACCATTTAGAGACGACGCTGCTGCAAGCGGCTTACCGCTCG	3179	Db	4200	GCTTCTGCTTTCTAGCGCGGCTGCTGCTGAGAGCGGCTTGTGGAGCATAGGCTTTGGG	4259
Qy	3181	CAGCGGCGAGGAGGAGTGTGAGGAGGAGTGGCAATTTACAGTTTGTGACTTCCAGGA	3240	Qy	4261	AAGGTGCTTGTGATATTTTGGCAGGTATATGGAGCAGGGGTGGCAGCGCGCTGCTGCC	4320
Db	3180	CAGCGGCGAGGAGGAGTGTGAGGAGGAGTGGCAATTTACAGTTTGTGACTTCCAGGA	3239	Db	4260	AAGGTGCTTGTGATATTTTGGCAGGTATATGGAGCAGGGGTGGCAGCGCGCTGCTGCC	4319
Qy	3241	GAACGGGCTTCCGGCATGTTCTGATTCCTCGTTCCTGCGAGTGTCTATGACGGGGTGT	3300	Qy	4321	TTTAAAGTCTATGAGCGCGGAGATGCCCTCCACCGAGGACCTTGGCTAACTTCTCTGCT	4380
Db	3240	GAACGGGCTTCCGGCATGTTCTGATTCCTCGTTCCTGCGAGTGTCTATGACGGGGTGT	3299	Db	4320	TTTAAAGTCTATGAGCGCGGAGATGCCCTCCACCGAGGACCTTGGCTAACTTCTCTGCT	4379
Qy	3301	GCTTGTGACAGCTCAGCCCGCGGACCTCAGTTAGTTGCGGGCTTACCTTAAACACA	3360	Qy	4381	ATCCTCTCCCTTGGCGCCCTAGTGTGCTGCGGAGCGGATCTGCTGCTGCGCAC	4440
Db	3300	GCTTGTGACAGCTCAGCCCGCGGACCTCAGTTAGTTGCGGGCTTACCTTAAACACA	3359	Db	4380	ATCCTCTCCCTTGGCGCCCTAGTGTGCTGCGGAGCGGATCTGCTGCTGCGCAC	4439
Qy	3361	CCAGGTTGCCGCTCCGAGGACCATCTGAGTTCTGGAGAGCGTCTTTACAGGCTC	3420	Qy	4441	GTGGGCGGAGGAGGCGGCTGTGCTGAGTGAACCGGCTGTATAGGCTTCTGCTTCCGG	4500
Db	3360	CCAGGTTGCCGCTCCGAGGACCATCTGAGTTCTGGAGAGCGTCTTTACAGGCTC	3419	Db	4440	GTGGGCGGAGGAGGCGGCTGTGCTGAGTGAACCGGCTGTATAGGCTTCTGCTTCCGG	4499
Qy	3421	ACCCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGAGGAGCAAACTTCCCTTAC	3480	Qy	4501	GGTAAACCAACGCTCTCCCCCAGCGCACTATGTGCTGTGAGAGCGGCTGTGAGCACTGTCT	4560
Db				Db	4500	GGTAAACCAACGCTCTCCCCCAGCGCACTATGTGCTGTGAGAGCGGCTGTGAGCACTGTCT	4559

QY	4561	CAGATCCCTCTCTAGTCTTTACCATCACTCAGCTGCTGAAGAGGCTTACACAGTGGATCAAC	4620
Db	4560	CAGATCCCTCTCTAGTCTTTACCATCACTCAGCTGCTGAAGAGGCTTACACAGTGGATCAAC	4619
QY	4621	GAGACTGCTCTCAAGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTGGGATTTGGATATGC	4680
Db	4620	GAGGATGCTCTCAAGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTGGGATTTGGATATGC	4679
QY	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCCTGCGCGGATTCGCGGA	4740
Db	4680	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCCTGCGCGGATTCGCGGA	4739
QY	4741	GTCCCTCTTCTCTCATGTCAAGCTGGGTACAAGGAGTCTGGCGGGCGACGGCATCATG	4800
Db	4740	GTCCCTCTTCTCTCATGTCAAGCTGGGTACAAGGAGTCTGGCGGGCGACGGCATCATG	4799
QY	4801	CAAAACCACTGCTCCATGTGGAGCAGATCAACCGGACATGTGAAAAAGGTTCCATGAGG	4860
Db	4800	CAAAACCACTGCTCCATGTGGAGCAGATCAACCGGACATGTGAAAAAGGTTCCATGAGG	4859
QY	4861	ATCGTGGGGCTAGGACTGTGTAGTAAACACGTTGGATGGAACATTTCCCAATTAACGCGTAC	4920
Db	4860	ATCGTGGGGCTAGGACTGTGTAGTAAACACGTTGGATGGAACATTTCCCAATTAACGCGTAC	4919
QY	4921	ACCACGGGCTGCTGACGCTCCCGGGCGCAAAATTTCTAGGGCGCTGTGGCGGGTG	4980
Db	4920	ACCACGGGCTGCTGACGCTCCCGGGCGCAAAATTTCTAGGGCGCTGTGGCGGGTG	4979
QY	4981	GCTGCTAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTCCACTAGTACGCGGCATG	5040
Db	4980	GCTGCTAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTCCACTAGTACGCGGCATG	5039
QY	5041	ACCACCTGACAAAGTAAAGTCCCGCTGTCAGCTGCAAAACCCCTCTACGGGAGGAGTGC	5100
Db	5040	ACCACCTGACAAAGTAAAGTCCCGCTGTCAGCTGCAAAACCCCTCTACGGGAGGAGTGC	5099
QY	5101	GATGGGTGCGGTGTCACAGTACGCTCCAGCTGCAAAACCCCTCTACGGGAGGAGTGC	5160
Db	5100	GATGGGTGCGGTGTCACAGTACGCTCCAGCTGCAAAACCCCTCTACGGGAGGAGTGC	5159
QY	5161	ACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTCAAGTCCCATCGAGCCCCGAA	5220
Db	5160	ACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTCAAGTCCCATCGAGCCCCGAA	5219
QY	5221	CCGAGCTAGCAGTGTCTACTTCATGCTCACCGACCCCTCCACATTAACGCGGACG	5280
Db	5220	CCGAGCTAGCAGTGTCTACTTCATGCTCACCGACCCCTCCACATTAACGCGGAGACG	5279
QY	5281	GCTAAGCTAGGTGGCCAGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
Db	5280	GCTAAGCTAGGTGGCCAGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5339
QY	5341	CTGCTGCGGCTTCTTGAAGCAACATGCTACCGTCAATGCTCCCGGACGCTGAC	5400
Db	5340	CTGCTGCGGCTTCTTGAAGCAACATGCTACCGTCAATGCTCCCGGACGCTGAC	5399
QY	5401	CTCATCGAGCCCACTCTCTGCGGCGCAGAGATGGCGGGAAACATCAACCGCTGGAG	5460
Db	5400	CTCATCGAGCCCACTCTCTGCGGCGCAGAGATGGCGGGAAACATCAACCGCTGGAG	5459
QY	5461	TCAGAAAAAAGGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGGAGGAGTGG	5520
Db	5460	TCAGAAAAAAGGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGGAGGAGTGG	5519
QY	5521	AGGGAAGTATTCCTTGGCGGAGATCTCGGAGGATTCAGGAAATTCCTCGAGCGATG	5580
Db	5520	AGGGAAGTATTCCTTGGCGGAGATCTCGGAGGATTCAGGAAATTCCTCGAGCGATG	5579
QY	5581	CCCATATGGGACGCGCGGATTAACACCTTCCACTGTAGTCTTGAAGTCCGAGGACCCGGAC	5640
Db	5580	CCCATATGGGACGCGCGGATTAACACCTTCCACTGTAGTCTTGAAGTCCGAGGACCCGGAC	5639

QY	5641	TACGTCCCTCCAGTGGTACACGGGTGTCCATTGCGCGCTGCAAGCGCCCTCCGATACCA	5700
Db	5640	TACGTCCCTCCAGTGGTACACGGGTGTCCATTGCGCGCTGCAAGCGCCCTCCGATACCA	5699
QY	5701	CCTCCACGGAGAAAGAGACGCTTCTCTGTCAGAACTCTACCGTCTCTCTGCTTGGG	5760
Db	5700	CCTCCACGGAGAAAGAGACGCTTCTCTGTCAGAACTCTACCGTCTCTCTGCTTGGG	5759
QY	5761	GAGTCTGCGCAAAAGACCTTTCGGCAGCTCCGAATCGTGGCGCTCGACAGCGGACGCA	5820
Db	5760	GAGTCTGCGCAAAAGACCTTTCGGCAGCTCCGAATCGTGGCGCTCGACAGCGGACGCA	5819
QY	5821	ACGGCTCTCTCTGACCGACCTTCCGACGACCGCGGATTCGAGTTCGCTGAC	5880
Db	5820	ACGGCTCTCTCTGACCGACCTTCCGACGACCGCGGATTCGAGTTCGCTGAC	5879
QY	5881	TCCTCCATGCCCCCTTTAGGGGAGCCGGGGATCCCGATCTCAGCGAGGGTCTTGG	5940
Db	5880	TCCTCCATGCCCCCTTTAGGGGAGCCGGGGATCCCGATCTCAGCGAGGGTCTTGG	5939
QY	5941	TCTACCGTAAAGCGAGGAGCTAGTGAAGACGCTGCTGCTGCTGCTGCTTACACATGG	6000
Db	5940	TCTACCGTAAAGCGAGGAGCTAGTGAAGACGCTGCTGCTGCTGCTGCTTACACATGG	5999
QY	6001	ACAGCGCCCTGATCAAGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060
Db	6000	ACAGCGCCCTGATCAAGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6059
QY	6061	AGCAACTCTTGTCTCCGTACCAACCTTGTCTATCTATCTATCTATCTATCTATCTATCT	6120
Db	6060	AGCAACTCTTGTCTCCGTACCAACCTTGTCTATCTATCTATCTATCTATCTATCTATCT	6119
QY	6121	CTGCGGAGAAAGGTCACCTTTTGAAGAGTTCAGAGTTCCTGAGGACCACTACCGGAC	6180
Db	6120	CTGCGGAGAAAGGTCACCTTTTGAAGAGTTCAGAGTTCCTGAGGACCACTACCGGAC	6179
QY	6181	GTGCTCAAGAGATGAAGGCGTCAAGTTCAGAGTTCCTGAGGACCACTACCGGAC	6240
Db	6180	GTGCTCAAGAGATGAAGGCGTCAAGTTCAGAGTTCCTGAGGACCACTACCGGAC	6239
QY	6241	GAAGCTGTAAAGTGTACGCGCCCACTTCGCGCAGATCTAAATTTGGCTATGGGCAAG	6300
Db	6240	GAAGCTGTAAAGTGTACGCGCCCACTTCGCGCAGATCTAAATTTGGCTATGGGCAAG	6299
QY	6301	GAGTCTCGGAACTATCCAGAAAGGCGTTAACCATTCGCTCCGCTGCGGAGGACCTG	6360
Db	6300	GAGTCTCGGAACTATCCAGAAAGGCGTTAACCATTCGCTCCGCTGCGGAGGACCTG	6359
QY	6361	CTGGAAGACACTGAGACCAATTTGACACCACTCATGCAAAATAGGTTTCTGCTG	6420
Db	6360	CTGGAAGACACTGAGACCAATTTGACACCACTCATGCAAAATAGGTTTCTGCTG	6419
QY	6421	GTCCAAACAGAGAGGCGGCGCAAGCGAGCTTCGCTTATCGTATTTCCAGATTTGGGG	6480
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Search completed: August 12, 2004, 04:08:49
Job time : 1852 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 03:20:41 ; Search time 12010 Seconds

(without alignments)

19871.653 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccgattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
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18: em_gss_inv:*
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20: em_gss_vrt:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	795.4	10.0	935	14	CK284786
2	794	9.9	804	14	CK291519
3	794	9.9	856	14	CK287297
4	794	9.9	910	14	CK287930

5	794	9.9	933	14	CK291799
6	794	9.9	936	14	CK256977
7	794	9.9	947	14	CK298208
8	794	9.9	954	14	CK283361
9	778.8	9.7	811	14	CK288185
10	587	7.3	878	14	CK288711
11	577.4	7.2	789	28	AQ361914
12	559.8	7.0	620	28	AQ398387
13	514.8	6.4	561	28	AQ447874
14	508	6.3	509	28	AQ447775
15	505.4	6.3	637	28	AQ447230
16	503.8	6.3	592	28	AQ449162
17	499	6.2	499	28	AQ398880
18	486.4	6.2	498	28	AQ398730
19	475.8	6.0	857	28	AQ875013
20	474.8	5.9	710	28	BH972732
21	469.8	5.9	473	28	AQ397768
22	468.8	5.9	594	28	AQ397253
23	465.2	5.8	850	28	AQ875052
24	463.4	5.8	798	28	AQ876139
25	458.8	5.7	482	9	AL449872
26	456.8	5.7	861	28	AQ875040
27	455.6	5.7	815	28	AQ876134
28	451.2	5.6	799	28	AQ876220
29	450	5.6	784	28	AQ876152
30	444.6	5.6	790	28	AQ875904
31	437.2	5.5	797	28	AQ876297
32	434.6	5.4	765	14	CK283362
33	426.8	5.3	804	28	AQ876080
34	422.8	5.3	759	14	CK298209
35	414.6	5.2	791	28	AQ876019
36	409.4	5.1	748	28	AQ501530
37	408	5.1	635	28	AQ447643
38	408	5.1	656	28	AQ447140
39	404	5.1	790	28	AQ875912
40	404	5.1	791	28	AQ876201
41	402.6	5.0	856	28	AQ875050
42	401.8	5.0	760	14	CK287931
43	398.8	5.0	722	14	CD641598
44	398	5.0	734	28	AQ873679
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ALIGNMENTS

CK284786 935 bp mRNA linear EST 15-DEC-2003
EST747508 Nicotiana benthamiana mixed tissue cDNA library.
normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5',
end, mRNA sequence.

CK284786
EST.

CK284786.1 GI:39858698

EST.

Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 935)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,

Staskiewicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST747509

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

FEATURES

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/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN
Query Match 10.0%; Score 795.4; DB 14; Length 935;
Best Local Similarity 99.9%; Pred. No. 6.1e-108; Indels 0; Gaps 0;
Matches 796; Conservative 0; Mismatches 1;

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DB 211 GCAGCAGCAGGCGAGCGGCTATCTGGCTGGCCACAGCGGCGGTTCTTGGCGAGCTGT 270
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LOCUS EST754233 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMC276 5',
end, mRNA sequence.
ACCESSION CK291519
VERSION CK291519.1 GI:39872047
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 804)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ART TAG GTG ACA CTA TAG.
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ORIGIN
Query Match 9.9%; Score 794; DB 14; Length 804;
Best Local Similarity 100.0%; Pred. No. 1e-107; Indels 0; Gaps 0;
Matches 794; Conservative 0; Mismatches 0;

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DB 62 CTATGACTGGGCAACAGACAATCGGCTGCTCTGATCGCGGCTTCCGGCTGTCAGC 121
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QY      629 CGACGTTGTTCACCTGAAGCGGGAAGGACTGGCTGCTATTGGCGGAAGTCCGGGGCAGGA 688
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QY      809 CGAGCAGCAGCAGTACTCGATGGAAGCGGCTCTTGTGATCAGATGATCTGACGAGGA 868
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VERSION    CK287297.1 GI:39863696
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST750020
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org

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Seq primer: ATT TAG GTG ACA CTA TAG.
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/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1169 CGAGTTCTTCTGAG 1182
Db 794 CGAGTTCTTCTGAG 807

RESULT 4
CK287930 910 bp mRNA linear EST 15-DEC-2003
LOCUS EST750652 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMBC75 5',
end, mRNA sequence.
ACCESSION CK287930
VERSION CK287930.1 GI:39864940
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST750653
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1. 910
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/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMBC75"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 9.9%; Score 794; DB 14; Length 910;
Best Local Similarity 100.0%; Pred. No. 9.9e-108;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGACAAAGATGATTGACGAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTCCG 448
Db 4 GATTGACAAAGATGATTGACGAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTCCG 63
QY 449 CTATGACTGGGCACAAACAGCAATCGGTCTCTGTATGCCGCGGTTCCTGCGCTGTACG 508
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Db 64 CTATGACTGGGCACAAACAGCAATCGGTCTCTGTATGCCGCGGTTCCTGCGCTGTACG 123
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Db 124 GCAGGGCGCGCCGGTCTTTTCTCAAGACCCGACCTGTTCGGTGCCTCGATCAATCAATGCA 183
QY 569 GGAACAGGACGCGCGCTATCGTGGTGGCCACGAGCGGCGTTCCTTTCGCGAGCTGTGCT 628
Db 184 GGAAGAGGACGCGCGCTATCGTGGTGGCCACGAGCGGCGTTCCTTTCGCGAGCTGTGCT 243
QY 629 CGACGTTGTCTACTGAAGCGGGAAGGAGCTGGTCTGCTATTGGGCGAAGTGGCGGGGAGGA 688
Db 244 CGACGTTGTCTACTGAAGCGGGAAGGAGCTGGTCTGCTATTGGGCGAAGTGGCGGGGAGGA 303
QY 689 TCTCCTGTCTATCTCACCTTCTCTCCGAGAAAGTATCATATGCTGCTGATGCAATGCG 748
Db 304 TCTCCTGTCTATCTCACCTTCTCTCCGAGAAAGTATCATATGCTGATGCAATGCG 363
QY 749 GCGGCTGCATACGCTTGTGATCCGCTACCTCCCATTCGACCAACGAGCAATCCGAT 808
Db 364 GCGGCTGCATACGCTTGTGATCCGCTACCTCCCATTCGACCAACGAGCAATCCGAT 423
QY 809 CGAGCGAGCAGTACTCGGATGGAAGCCGCTTCTGTCGATCAGGATGATCTGGACGAGA 868
Db 424 CGAGCGAGCAGTACTCGGATGGAAGCCGCTTCTGTCGATCAGGATGATCTGGACGAGA 483
QY 869 GCATCAGGGCTCGCGCCAGCCGACCTGTCGAGCTCAAGGCGGCGCATGCCCGACGG 928
Db 484 GCATCAGGGCTCGCGCCAGCCGACCTGTCGAGCTCAAGGCGGCGCATGCCCGACGG 543
QY 929 CGAGGATCTCGTCTGTGACCCATCGCGATGCTGCTCCGAAATATCATGTTGGGAAAATGG 988
Db 544 CGAGGATCTCGTCTGTGACCCATCGCGATGCTGCTCCGAAATATCATGTTGGGAAAATGG 603
QY 989 CCGCTTTTCTGGATTTCATGACTGTGCGCGCTGGTGTGCGGACCGCTATCAGGACAT 1048
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QY 1049 AGCGTTGGCTACCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCT 1108
Db 664 AGCGTTGGCTACCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCT 723
QY 1109 CGTGCTTTACGGTATCGCCGCTCCCGATTCCGAGCGCATCGCCTTCTATCGCCTTCTTGA 1168
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QY 1169 CGAGTTCTTCTGAG 1182
Db 784 CGAGTTCTTCTGAG 797

RESULT 5
CK291799 933 bp mRNA linear EST 15-DEC-2003
LOCUS EST754513 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMC477 5',
end, mRNA sequence.
ACCESSION CK291799
VERSION CK291799.1 GI:39872608
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST754514
Contact: Robin Buell
The Institute for Genomic Research
```


9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
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 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
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 /clone="NBMCA477"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 tissues: RNA was isolated from Nicotiana benthamiana
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;
 Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 14; Length 933;
 Best Local Similarity 100.0%; Pred. No. 9.8e-108;
 Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAGATGGATTGACGAGGTTCTCGCGCGTTGGTGAGAGGCTATTCCG 448
 Db 46 GATTGAACAGATGGATTGACGAGGTTCTCGCGCGTTGGTGAGAGGCTATTCCG 105

QY 449 CTATGACTGGGCAACAGACAATCGGCTCTGTATCGCGCGTTTCGGCTGTGAGC 508
 Db 106 CTATGACTGGGCAACAGACAATCGGCTCTGTATCGCGCGTTTCGGCTGTGAGC 165

QY 509 GCAGGGGCGCGGTTCTTTTGTCTAAGACCGACCTGTTCGGTGCCTGAATGAATGCA 568
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QY 569 GGACGAGGCGAGCGGCTATCGTGGTGGCCAGCGAGGCTTCCTTGGCGAGCTGTGCT 628
 Db 226 GGACGAGGCGAGCGGCTATCGTGGTGGCCAGCGAGGCTTCCTTGGCGAGCTGTGCT 285

QY 629 CGACGTTGTCTAAGAGCGGGAAGGACTGGTGTCTATTGGCGAAGTGCCTGGGCGAGCA 688
 Db 286 CGACGTTGTCTAAGAGCGGGAAGGACTGGTGTCTATTGGCGAAGTGCCTGGGCGAGCA 345

QY 689 TCTCTGTCTATCTCACTTGTCTTCTCCGAGAAATATCATCATCTGATGCAATGCG 748
 Db 346 TCTCTGTCTATCTCACTTGTCTTCTCCGAGAAATATCATCATCTGATGCAATGCG 405

QY 749 CGCGGTGCTATGCTTGTATCGCGCTACCTGCCATTCGACCAACGAGCAATCGCAT 808
 Db 406 CGCGGTGCTATGCTTGTATCGCGCTACCTGCCATTCGACCAACGAGCAATCGCAT 465

QY 809 CGAGCGAGCACTATCTGATGGAAGCGGTTCTTGTGATCAGGATGATCTGAGCAAGA 868
 Db 466 CGAGCGAGCACTATCTGATGGAAGCGGTTCTTGTGATCAGGATGATCTGAGCAAGA 525

QY 869 GCATCAGGGGCTCGCGCGAGCAATGTTTCGCCAGGCTCAAGGCGCGATGCCGACGG 928
 Db 526 GCATCAGGGGCTCGCGCGAGCAATGTTTCGCCAGGCTCAAGGCGCGATGCCGACGG 585

QY 929 CGAGGATCTCGTGTGACCCATGGCGATGCGCTTGTGCGAATATCATGCTGGAATGCG 988
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QY 989 CGGCTTTCTGGAATTCAGACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 1048

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 QY 1049 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCGAATGGCTGACCGCTTCT 1108
 Db 706 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCGAATGGCTGACCGCTTCT 765

QY 1109 CGTCTTTACGGTATCGCGCTCCCGATTCGACGCGCATCGCTTCTATCGCCTTCTTGA 1168
 Db 766 CGTCTTTACGGTATCGCGCTCCCGATTCGACGCGCATCGCTTCTATCGCCTTCTTGA 825

QY 1169 CGAGTCTTCTTCTGAG 1182
 Db 826 CGAGTCTTCTTCTGAG 839

RESULT 6
 CK256977
 LOCUS
 DEFINITION
 ESR740614 potato callus cDNA library, normalized and full-length
 Solanum tuberosum cDNA clone POC170 5' end, mRNA sequence.
 CK256977
 VERSION
 CK256977.1 GI:39813957
 KEYWORDS
 EST
 SOURCE
 Solanum tuberosum (potato)
 ORGANISM
 Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.
 REFERENCE
 1 (bases 1 to 936)
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
 Generation of ESTs from potato callus tissue
 Unpublished (2003)
 CONTACT: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
 source
 1. .936
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POCD170"
 /tissue_type="callus"
 /lab_host="DH10B-Tona"
 /clone_lib="potato callus cDNA library, normalized and
 full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Solanum tuberosum var.
 Kennebec callus tissue grown on solid media."

ORIGIN
 Query Match 9.9%; Score 794; DB 14; Length 936;
 Best Local Similarity 100.0%; Pred. No. 9.8e-108;
 Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAGATGGATTGACGAGGTTCTCGCGCGGTTGGTGAGAGGCTATTCCG 448
 Db 14 GATTGAACAGATGGATTGACGAGGTTCTCGCGCGGTTGGTGAGAGGCTATTCCG 73

QY 449 CTATGACTGGGCAACAGACAATCGGCTCTGTATCGCGCGGCTTCGGCTGTGAGC 508
 Db 74 CTATGACTGGGCAACAGACAATCGGCTCTGTATCGCGCGGCTTCGGCTGTGAGC 133

QY 509 CGAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTTCGGTGCCTGAATGAATGCA 568
 Db 134 CGAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTTCGGTGCCTGAATGAATGCA 193

QY 569 CGAGGAGGCGGCTATCGTGGTGGCGGCGCTTCTTGGCGAGCTGTGCT 628


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Db      737  CGTGTCTTACGGTATCGCGCTCCGATCGCAGCGCATCGCTTCTATCGCCTTCTTGA 796
QY      1169  CGAGTTCTTCTGAG 1182
Db      797  CGAGTTCTTCTGAG 810

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LOCUS   EST746083 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMAG50 5',
end, mRNA sequence.
ACCESSION CK283361
VERSION   CK283361.1 GI:39855898
KEYWORDS  EST.
SOURCE   Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 954)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
           Staskawicz,B., Jin,H. and Baker,B.
TITLE     Generation of EST sequences from Nicotiana benthamiana
JOURNAL   Unpublished (2003)
COMMENT   Other ESTs: EST746084
           Contact: Robin Buell
           The Institute for Genomic Research
           9712 Medical Center Dr, Rockville, MD 20850, USA
           Email: potato-array@tigr.org
           Clones can be requested from TIGR via potato@tigr.org
           Seq primer: ATT TAG CTG ACA CTA TAG.
FEATURES  Location/Qualifiers
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               callus tissue and root tissue"
               /lab_host="DH10B-TonA"
               /clone_lib="Nicotiana benthamiana mixed tissue cDNA
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               /note="Vector: pCMVSPORT6.1; Site.1: EcoRI; Site.2: NotI;
               supplier: RNA was isolated from Nicotiana benthamiana
               tissues that include callus, roots from liquid culture
               grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
               cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
               challenged leaves (Pseudomonas syringae pv tomato 12 hr;
               Xanthomonas campestris pv campestris 12 hr, 18hr;
               Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
               campestris pv vesicatoria 18hr). RNA was isolated from
               these tissues and pooled in approximately equal molar
               amounts."
ORIGIN
Query Match 9.9%; Score 794; DB 14; Length 954;
Best Local Similarity 100.0%; Pred. No. 9.7e-108;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      389  GATTGAACAAGATGGATTGCAGCAGGTTCTCCGCCGCTTGGGGAGAGGCTATTGG 448
Db      14   GATTGAACAAGATGGATTGCAGCAGGTTCTCCGCCGCTTGGGGAGAGGCTATTGG 73
QY      449  CTATGACTGGGCACACACAGCAATCGGTCTCTGATGCCGCCGTGTTCGGCTGTGAGC 508
Db      74   CTATGACTGGGCACACACAGCAATCGGTCTCTGATGCCGCCGTGTTCGGCTGTGAGC 133
QY      509  GCAGGGGCGCGCGTCTTTTGTCAAGACCGACTGTCCGGTGCCCTGAATGAATGCA 568
Db      134  GCAGGGGCGCGCGTCTTTTGTCAAGACCGACTGTCCGGTGCCCTGAATGAATGCA 193

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QY      569  GGACGAGGAGCGCGGCTATCGTGGCTGGCCACGACGGCGTTCCTTTGCGCAGCTGTGCT 628
Db      194  GGACGAGGAGCGCGGCTATCGTGGCTGGCCACGACGGCGTTCCTTTGCGCAGCTGTGCT 253
QY      629  CGACGTTGTCACTGAAGCGGGAAGGAGCTGGCTCTATTGGGGCGAAGTGCCTGGGGGAGGA 688
Db      254  CGACGTTGTCACTGAAGCGGGAAGGAGCTGGCTCTATTGGGGCGAAGTGCCTGGGGGAGGA 313
QY      689  TCTCTGTCTATCTCACCTTCTCTCCGAGAAAGTATCCATCATGCTCATGCAATGCG 748
Db      314  TCTCTGTCTATCTCACCTTCTCTCCGAGAAAGTATCCATCATGCTCATGCAATGCG 373
QY      749  GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACACCACCAAGCGAAATCATGCGAT 808
Db      374  GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACACCACCAAGCGAAATCATGCGAT 433
QY      809  CGAGCGGAGCAGCTACTCGGATGGAAGCCGCTCTTTCGATCAGGATGATCTGGACGAAGA 868
Db      434  CGAGCGGAGCAGCTACTCGGATGGAAGCCGCTCTTTCGATCAGGATGATCTGGACGAAGA 493
QY      869  GCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGACGGCTCAAGCGCGCATGCCGACGG 928
Db      494  GCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGACGGCTCAAGCGCGCATGCCGACGG 553
QY      929  CGAGGATCTCTGCTGATGCCATGGCGATGCTGCTTTCGCGAATATCATGCTGGAAATGG 988
Db      554  CGAGGATCTCTGCTGATGCCATGGCGATGCTGCTTTCGCGAATATCATGCTGGAAATGG 613
QY      989  CGCTTTTCTGGATTCATGACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 1048
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QY      1049  AGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGCGAATGGCTGACCGCTTCTCT 1108
Db      674  AGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGCGAATGGCTGACCGCTTCTCT 733
QY      1109  CGTGTCTTACGGTATCGCGCTCCCGATTCCGAGCATCGCTTCTATCGCCTTCTTGA 1168
Db      734  CGTGTCTTACGGTATCGCGCTCCCGATTCCGAGCATCGCTTCTATCGCCTTCTTGA 793
QY      1169  CGAGTTCTTCTGAG 1182
Db      794  CGAGTTCTTCTGAG 807

CK288185      811 bp mRNA linear EST 15-DEC-2003
EST750907 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMBE61 5',
end, mRNA sequence.
CK288185
CK288185.1 GI:39865462
EST.
SOURCE   Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 811)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
           Staskawicz,B., Jin,H. and Baker,B.
TITLE     Generation of EST sequences from Nicotiana benthamiana
JOURNAL   Unpublished (2003)
COMMENT   Contact: Robin Buell
           The Institute for Genomic Research
           9712 Medical Center Dr, Rockville, MD 20850, USA
           Email: potato-array@tigr.org
           Clones can be requested from TIGR via potato@tigr.org
           Seq primer: ATT TAG CTG ACA CTA TAG.
FEATURES  Location/Qualifiers
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             1..811

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/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."
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Query Match 9.7%; Score 778.8; DB 14; Length 811;
Best Local Similarity 99.7%; Pred. No. 1.8e-105;
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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90 CGGTATGACTGGGCACACAGACAAATCGGTCTCTGATCCGCGCGTGTCCGGCTGTC 149
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210 GCAGGACGAGCAGCGCGCTATCGTGGTGGCAGCGGCTTCTTGGCAGCTGT 269
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Qy 626 GCTGACCTGTCTCAAGGAGGAGGAGTGGCTGTATTGGCGGAAGTGGCGGGCA 685
Db |||
270 GCTGACCTGTCTCAAGGAGGAGGAGTGGCTGTATTGGCGGAAGTGGCGGGCA 329
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Qy 686 GATCTCTGTCTCATCTGCTTCTTCCGAGAAAGTATCATATGGCTGTGCAAT 745
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330 GATCTCTGTCTCATCTGCTTCTTCCGAGAAAGTATCATATGGCTGTGCAAT 389
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Qy 746 GCGCGGCTGCTATGCTTGTATCGGCTTACCTGCCCTTCCGACCAAGCGAATCATCG 805
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Qy 806 CATGAGCGAGCAGCTGCTGATGAGAGCGGCTTGTGATCAGGATGATCTGAGCA 865
Db |||
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Qy 1166 TG 1167
Db ||
810 TG 811
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RESULT 10
CK288711 878 bp mRNA linear EST 15-DEC-2003
LOCUS EST751433 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalised, full-length Nicotiana benthamiana cDNA clone NMBB149 5',
end, mRNA sequence.
ACCSSION CK288711
VERSION CK288711.1 GI:398666496
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 878)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NMBB149"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN
Query Match 7.3%; Score 587; DB 14; Length 878;
Best Local Similarity 100.0%; Pred. No. 4.2e-77;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 596 GSCCAGCAGCGGCGTCTCTTGGCAGCTGTGTCGACGTTGTCACTGAAGCGGAGGGA 655
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1 GSCCAGCAGCGGCGTCTCTTGGCAGCTGTGTCGACGTTGTCACTGAAGCGGAGGGA 60
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Db |||
61 CTGGCTGTCTATTGGCGAAGTCCCGGGCAGATCTCTGTGATCTACCTTGTCTCTGC 120
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Qy 716 CGAGAAAGTATCCATGCTGATGCGGCTGATGCGGCTGATGCTGATGCTGCTGCTAC 775
Db |||

Db 121 CGAGAAAGTATCCATCATGGCTGATCAATGCGCGCTGCATACGCTTGTATCCGGCTAC 180

QY 776 CTGCCATTGACCCACCAAGCAAAATCGATCGAGCGAGGACGCTACTCGGATGGAAGC 835

Db 181 CTGCCATTGACCCACCAAGCAAAATCGATCGAGCGAGGACGCTACTCGGATGGAAGC 240

QY 836 CGGTCTTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAAT 895

Db 241 CGGTCTTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAAT 300

QY 896 GTTCCGAGGCTCAAGCGCGGATGCGGACGCGAGGATCTGCTGATGACCAAGCGGA 955

Db 301 GTTCCGAGGCTCAAGCGCGGATGCGGACGCGAGGATCTGCTGATGACCAAGCGGA 360

QY 956 TGCCTGCTTGGCGGAATATCATGTTGGAATATGCGCGCTTTCTGATTCATGACGCTGG 1015

Db 361 TGCCTGCTTGGCGGAATATCATGTTGGAATATGCGCGCTTTCTGATTCATGACGCTGG 420

QY 1016 CCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGTACCCGCTGATATTCGTA 1075

Db 421 CCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGTACCCGCTGATATTCGTA 480

QY 1076 AGAGCTTGGCGGGAATGGGCTGACCGCTTCCTGCTGCTTTACGATACCGCGCTCCGA 1135

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Db 541 TTTCGAGCGCATCGCTTCTATCGCCTCTCTGACGAGTTCTTCTGAG 587

RESULT 11

AQ361914

LOCUS

DEFINITION

clone mgxb0005K01f, genomic survey sequence.

ACCESSION

VERSION

AQ361914.1 GI:4211753

KEYWORDS

GSS.

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 789)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGATCACTATAGGG

Class: BAC ends

High quality sequence start: 41

High quality sequence stop: 392.

Location/Qualifiers

FEATURES

source

1..789

/organism="Magnaporthe grisea"

/mol_type="genomic DNA"

/strain="70-15"

/db_xref="taxon:148305"

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/tissue_type="Protoplasts"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;

Rice blast is one of the most devastating fungal diseases

of rice world wide. It is a filamentous ascomycete with

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

Query Match 7.2%; Score 577.4; DB 28; Length 789;

Best Local Similarity 97.8%; Pred. No. 1.1e-75;

Matches 584; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 581 GCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGGCGAGCTGTCTCGAGCTTCAC 640

Db 39 GNGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGGCGAGCTGTCTCGAGCTTCAC 98

QY 641 TGAAGCGGGAAGGAGTGGCTGCTATTGGGCGAAGTGC CGGGCGAGGATCTCTGTGATC 700

Db 99 TGAAGCGGGAAGGAGTGGCTGCTATTGGGCGAAGTGC CGGGCGAGGATCTCTGTGATC 158

QY 701 TCACCTTGTCTTGGCGGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGCATAC 760

Db 159 TCACCTTGTCTTGGCGGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGCATAC 218

QY 761 GTTGATCGGCTACTCTGCCATTTCGACCAAGCGAAATCGCATCGAGCGAGCAGC 820

Db 219 GTTGATCGGCTACTCTGCCATTTCGACCAAGCGAAATCGCATCGAGCGAGCAGC 278

QY 821 TACTCGGATGGAAGCGGCTTGTTCGATCAGATGATCTGGAGGAGAGCATCAGGGCT 880

Db 279 TACTCGGATGGAAGCGGCTTGTTCGATCAGATGATCTGGAGGAGAGCATCAGGGCT 338

QY 881 CGCGCAGCCGAACCTGTTCCGCGAGCTCAAGCGCGCATGCCCGCGAGGATCTCGT 940

Db 339 CGCGCAGCCGAACCTGTTCCGCGAGCTCAAGCGCGCATGCCCGCGAGGATCTCGT 398

QY 941 COTGACCATGCGATGCTGTTCCGGAATATCATGTTGGAAATGCGCGCTTTCTCG 1000

Db 399 COTGACCATGCGATGCTGTTCCGGAATATCATGTTGGAAATGCGCGCTTTCTCG 458

QY 1001 ATTCACTGCTGCGCGCTGGGTGGCGAGCGCTATCAGGACATAGCGTTGGCTAC 1060

Db 459 ATTCACTGCTGCGCGCTGGGTGGCGAGCGCTATCAGGACATAGCGTTGGCTAC 518

QY 1061 CCGTGATATTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGCTTTACGG 1120

Db 519 CCGTGATATTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGCTTTACGG 578

QY 1121 TATCGCGCTCCGATTCGAGCGCATCGCTTCTATCGCTTCTTACGAGTTCTT 1177

Db 579 TATCGCGCTCCGATTCGCAACGATTCGCTTCTATCGGCTTTTGGAGGNTTTT 635

RESULT 12

AQ398387

LOCUS

DEFINITION

clone mgxb0009J05f, genomic survey sequence.

ACCESSION

VERSION

AQ398387.1 GI:4369414

KEYWORDS

GSS.

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 620)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGATCACTATAGGG

Class: BAC ends

High quality sequence start: 41

High quality sequence stop: 392.

Location/Qualifiers

COMMENT

Contact: Dean RA
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 187.
Location/Qualifiers
1. .620

FEATURES

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/organism="Magnaporthe grisea"
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/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 7.0%; Score 559.8; DB 28; Length 620;
Best Local Similarity 98.8%; Pred. No. 4.8e-73;
Matches 564; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

609 GTTCTTGGCAGCTGCTCGAGTGTCTACTGAAGCGGGAAGGAGTGGCTGCTATTG 668
Db 1 GTTCTTGGCAGCTGCTCGAGTGTCTACTGAAGCGGGAAGGAGTGGCTGCTATTG 60
669 GGCGAAGTGGCGGGCAGGATCTCTGTCACTCACCTTGTCTCTGCGGAGAAAGTATCC 728
Db 61 GGCGAAGTGGCGGGCAGGATCTCTGTCACTCACCTTGTCTCTGCGGAGAAAGTATCC 120
729 ATCATGGCTGATCAATGCGGCGGTGCATACGCTTGATCGGCTACTCGCCATTTGAC 788
Db 121 ATCATGGCTGATCAATGCGGCGGTGCATACGCTTGATCGGCTACTCGCCATTTGAC 180
789 CACCAAGCGAATCATCGATCGAGCGACGCTACTCGATGGAAGCGGTCTTGTGAT 848
Db 181 CACCAAGCGAATCATCGATCGAGCGACGCTACTCGATGGAAGCGGTCTTGTGAT 240
849 CAGGATGATCTGGAGAAAGAGCATCAGGGGCTCGCGCCAGCCGAACTTTTCGCCAGGCTC 908
Db 241 CAGGATGATCTGGAGAAAGAGCATCAGGGGCTCGCGCCAGCCGAACTTTTCGCCAGGCTC 300
909 AAGGCGGCATGCCCGAGCGGAGGATCTCGTGTGACCCATGGCGATGCTGCTGGCG 968
Db 301 AAGGCGGCATGCCCGAGCGGAGGATCTCGTGTGACCCATGGCGATGCTGCTGGCG 360
969 AATATCATGGTGGAAATGGCGCTTTCTGATTCATCGACTGTGGCGCGCTGGGTGTG 1028
Db 361 AATATCATGGTGGAAATGGCGCTTTCTGATTCATCGACTGTGGCGCGCTGGGTGTG 420
1029 CGCGACCGCTATCAGGACATAGCGTTGGTACCCGTGATATGTCGAAGAGCTTGGCGGC 1088
Db 421 CGCGACCGCTATCAGGACATAGCGTTGGTACCCGTGATATGTCGAAGAGCTTGGCGGC 480
1089 GAATGGGCTGACCGCTTCTCTGTGCTTACGGTATCGCGCTCCGATTCGACGGCATC 1148
Db 481 GAATGGGCTGACCGCTTCTCTGTGCTTACGGTATCGCGCTCCGATTCGACGGCATC 540

QY

1149 GCCTTCTATCGCCTCTTTGACGAGTTCTTCT 1179

Db

541 GCCTTCTATCGCCTCTTTGACGAGTTTCTT 571

RESULT 13

LOCUS

DEFINITION

AQ447874 561 bp DNA linear GSS 08-APR-1999
mgxb0012101f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0012101f, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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QY 750 CGGCTGATACGCTGTGATCCGGCTACCTGCGCATTCGACCAACGAGAAACATCGCATC 809
Db 284 CGGCTGATACGCTGTGATCCGGCTACCTGCGCATTCGACCAACGAGAAACATCGCATC 343
QY 810 GAGCGAGCAGTACTCGGATGGAAGCGGCTCTGTCGATCAGGATGATCTGAGCAAGAG 869
Db 344 GAGCGAGCAGTACTCGGATGGAAGCGGCTCTGTCGATCAGGATGATCTGAGCAAGAG 403
QY 870 CATCAGGGGCTCGCGCAGCGAACTGTTCGCGAGGCTCAAGGCGCGCATCGCGACGGC 929
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QY 930 GAGGATCTGCTGCGACCCATGGCGATGCGCTGTCGCGAATATCATGTTGGAAATGGC 989
Db 464 GAGGATCTGCTGCGACCCATGGCGATGCGCTGTCGCGAATATCATGTTGGAAATGGC 523
QY 990 CGCTTTTCTGGATTATCATGACTGTGGCGCGCTGGGTGT 1027
Db 524 CGCTTTTCTGGATTATCATGACTGTGGCGCGCTGGGTGT 561

A0447775 509 bp DNA linear GSS 08-APR-1999
mgxb0011E13f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0011E13f, genomic survey sequence.
A0447775
GSS.
A0447775.1 GI:4576912
Magnaporthe grisea (anamorph: Pyricularia grisea)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence stop: 342.
Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="mgxb0011E13f"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
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blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters

```

are available upon request."

Query Match 6.4%; Score 508; DB 28; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.3e-65;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 629 CGAGTTTGTCTACTGAACGGGAGGAGCTGGCTCTATTGGCGAAAGTGGCGGGCAGGA 688
Db 1 CGAGTTTGTCTACTGAACGGGAGGAGCTGGCTCTATTGGCGAAAGTGGCGGGCAGGA 60
QY 689 TCTCTCTCATCTCACCTCTGCTCTGCGGAGAAAGTATCCATCATGGCTGATGCAATGCG 748
Db 61 TCTCTCTCATCTCACCTCTGCTCTGCGGAGAAAGTATCCATCATGGCTGATGCAATGCG 120
QY 749 GCGGCTGATACGCTTGTGATCCGGCTACCTGCCCATTCGACCAACGCGGAAACATCGCAT 808
Db 121 GCGGCTGATACGCTTGTGATCCGGCTACCTGCCCATTCGACCAACGCGGAAACATCGCAT 180
QY 809 CGAGCGAGCAGCTACTCGGATGGAAGCGGCTCTTGTGATCAGGATGATCTGAGCAAGA 868
Db 181 CGAGCGAGCAGCTACTCGGATGGAAGCGGCTCTTGTGATCAGGATGATCTGAGCAAGA 240
QY 869 GCATCAGGGGCTCGCGCAGCGCAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCGACGG 928
Db 241 GCATCAGGGGCTCGCGCAGCGCAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCGACGG 300
QY 929 CGAGGATCTGCTGTCGATGACCCATGCGCATGCTCTTGCAGAAATATCATGTTGAAATGG 988
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QY 989 CGGCTTTTCTGGATTATCATGCTGGCGGCTGGGTGTGGCGACCGCTATCAGGACAT 1048
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QY 1049 AGCGTTTGGCTACCGCTGATATTCGCAAGAGCTTGGCGGGAATGGCTGACCGTTTCT 1108
Db 421 AGCGTTTGGCTACCGCTGATATTCGCAAGAGCTTGGCGGGAATGGCTGACCGTTTCT 480
QY 1109 CGTGTCTTTCAGGATGATCGCGCTCCCGAT 1136
Db 481 CGTGTCTTTCAGGATGATCGCGCTCCCGAT 508

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A0447230 637 bp DNA linear GSS 08-APR-1999
mgxb0006O09f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0006O09f, genomic survey sequence.

A0447230
GI:4576367

GSS.

Magnaporthe grisea (anamorph: Pyricularia grisea)

Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 637)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCACTATAGG

Class: BAC ends

High quality sequence stop: 291.

Location/Qualifiers

FEATURES

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/clone_lib="CUGI Rice Blast BAC Library"
/notes="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
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order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN
Query Match 6.3%; Score 505.4; DB 28; Length 637;
Best Local Similarity 99.8%; Pred. No. 5.3e-65;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 676 TGCCGGGCGCAGGATCTCTGTGTCATCTACCTTGCTCTCGCGGAGAAAGTATCCATCATGG 735
Db 1 TGCCGGGCGCAGGATCTCTGTGTCATCTACCTTGCTCTCGCGGAGAAAGTATCCATCATGG 60

Qy 736 CTGATGCAATCGGGCGGTGTCATCGGTTGATCGGCTACCTGCCATTCGACACCAAG 795
Db 61 CTGATGCAATCGGGCGGTGTCATCGGTTGATCGGCTACCTGCCATTCGACACCAAG 120

Qy 796 CGAAACATCGGATCGAGCGAGCAGCTACTCGGATCGAAGCCGGTCTTGTGATCAGGATG 855
Db 121 CGAAACATCGGATCGAGCGAGCAGCTACTCGGATCGAAGCCGGTCTTGTGATCAGGATG 180

Qy 856 ATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGAGGCTCAAGGGCC 915
Db 181 ATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGAGGCTCAAGGGCC 240

Qy 916 GCATGCCCGCGCGGAGCATCTCGTCTGTCACCCATGGGATGCTGTCGCGAATATCA 975
Db 241 GCATGCCCGCGCGGAGCATCTCGTCTGTCACCCATGGGATGCTGTCGCGAATATCA 300

Qy 976 TGGTGGAAAAATGGCGGCTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACC 1035
Db 301 TGGTGGAAAAATGGCGGCTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACC 360

Qy 1036 GCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAAGAGCTTGGCGGGAATGGG 1095
Db 361 GCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAAGAGCTTGGCGGGAATGGG 420

Qy 1096 CTGACGGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTCCGAGCGCATCGCCTTCT 1155
Db 421 CTGACGGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTCCGAGCGCATCGCCTTCT 480

Qy 1156 ATCGGCTTCTTGACGAGTTCTTCTGAG 1182
Db 481 ATCGGCTTCTTGACGAGTTCTTCTGAG 507
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Job time : 12016 secs